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## ALIGNMENTS

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New nucleic acid encoding human transcription factor IIIA, useful for treatment and diagnosis of cancer and inherited disease $\cdot$	WPI; 2000-387419/33.	Bordon-Pallier F, Rocher C;	(HMRI ) HOECHST MARION ROUSSEL.	10-NOV-1998; 98FR-0014146.	09-NOV-1999; 99WO-FR02738.	18-MAY-2000.	WO200028024-A1.	Homo sapiens.	cancer; ss.	transcription; ribosomal RNA 5S gene; transcriptional control;	Human; transcription factor; htfIIIA; DNA-binding protein;	Fragment of DNA encoding a transcription factor designated htfIIIA.	04-SEP-2000 (first entry)		AAA15407;	RESULT 1 AAA15407 ID AAA15407 standard; DNA; 1213 BP.

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Query Match
Best Local Similarity
Matches 1213; Conserv
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Matches 1212; Conserv
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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The concern cantigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the preventic diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention
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                                               Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                       adult respiratory distress syndrome; inflammatory bowel d
Crohn's disease; ulcerative colitis; periodontal disease;
                                                                                                                                                                                                                                                                                                                                             fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; ARDS; cardiac reperfusion injury; ARDS;
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                                                            detecting differential expression e activation, which serves as
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CO DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC dC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC level of expression of the gene is indicative of inflammation;
CC et a pathogen or sterile inflammatory disease, by detecting the
CC level of expression of the gene is indicative of inflammation;
CC an allergic response in a subject, exposure of a
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating CA; M2 is useful for exponsion of an aneant canable of modulating
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                                                               CAAGCACACGGGGGAGAGACCATTTGTTTGTGACTATGAAGGGTGTGGCAAGGCCTTCAT
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by detecting the level of expression of gene(s) (Gs) identified
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Pred. No. 2.4e-303;
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## AAT14038 standard; cDNA;

07-JUL-1996

(first

entry)

Human; transcription factor-IIIA; hTFIIIA; DNA binding protein; ribosome; zinc finger; rapid amplification of cDNA ends; 5'-RAC primer; PCR; polymerase chain reaction; foetal brain; anchor primer; diagnostic; probe; transcription control; HOMO Transcription factor-IIIA gene. sapiens cancer; probe; transcription control;

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                                                                                                                                                                                                                                                                                    The sequence encodes human transcription factor-IIIA (hTFIIIA), a DNA binding protein with 9 zinc finger domains, which is necessary for the initiation of 55 RNA gene transcription, binding to an internal control region of the 55 gene. The coding region internal control region of the 55 gene. The coding region of colaimed) is given in AAT14037. A fragment lacking a 5'-portion of the gene has been isolated from a human foetal brain cDNA library internal control of cDNA ends using primers H11-R (AAT14039), complementary to anchor primer AAT14041). Reverse transcription using H-1R is anchor primer AAT14041. Reverse transcription using H-1R is collowed by anchor primer ligation and PCR using AP-2 and H11-E, to give a full-length cDNA, OTK7. The gene and its encoded protein cD may be used in diagnossis, identification or therapy of hereditary collabeases such as cancer, or other diseases resulting from abnormal transcriptional control, and to analyse the mechanisms involved in
                                                                                                                                                                                                                                    Query Match
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CTCCTTCCCTGACTGCAGCGCCAATTACAGCAAAGCCTGGAAGCTTGACGCGCACCTGTG
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                                     AGCCGGCGAGAGCTCAGCTCCGACCCCGCGCGCCCCGCGCTTCCCAGGAGGTTCATCTG
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                                                                                                                                                                                                           The sequence encodes human transcription factor-IIIA (hTFIIIA), and binding protein with 9 zinc finger domains, which is necessary for the initiation of 55 RNA gene transcription, binding to an internal control region of the 55 gene. A fuller cDNA sequence with flanking regions is given in AAT14038. A fragment lacking a CC with flanking regions is given in AAT14038. A fragment lacking a CC cDNA library (OTK7-1), and the 5'-portion of the gene has been isolated from a human foetal brain CC cDNA library (OTK7-1), and the 5'-portion of the gene has been isolated by 5'-rapid amplification of cDNA ends using primers H11-R (CC (AAT14039), H11-E (AAT14040), H11-H (AAT14043). Reverse transcription using CC (H1R is followed by anchor primer ligation and PCR using AP-2 and CC H11-E, to give a full-length cDNA, OTK7. The gene and its encoded CC protein may be used in diagnossis, identification or therapy of hereditary diseases such as cancer, or other diseases resulting from abnormal transcriptional control, and to analyse the mechanisms
                                                                                                                                                   Query Match
Best Local Sim
Matches 1203;
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The invention relates to 2175 novel human ovarian antigens (ABP41054-CC ABP4328) and to CDNAs encoding them (ABP5431-ABP656305), and also CC encompasses polypeptides 90% identical and polynucleotides 95% identical CC to the sequences of the invention. The invention additionally relates to CC recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use CC of ovarian antigen polynucleotides and polypeptides in diagnosing. CC treating, prognosing or preventing various ovary and/or breast-related CC disorders. Such conditions include ovarian cancer and breast cancer, and CC metastatic tumours of ovarian or breast origin, reproductive system CC disorders (e.g., infertility, disorders of pregnancy, anovulation, CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic CC shock syndrome), inflammatory conditions (e.g., mastitis, cophoritis and CC usainitis), immine disorders (e.g., congenital and acquired conditions (e.g., mastitis, systemic lupus erythematosus), CC blood-related disorders (e.g., congenital and acquired disorders, neurological disorders, gastrointestinal disorders CC and urinary system disorders. Ovarian antigen polypeptides and CC computate ovarian antigen polypeptides and CC compounds which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; ovarian antigen; ovary; ovarian; breast, concer; cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrom PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; harnow; chromosome mapping; forensic analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurological diseases
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                                                                                 modulate ovarian antigen expression or activity. The polynucleotides
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                                           further be used for gene therapy, chromosome mapping, identification of individuals and in forensic analysis
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reproductive; chromosome 13q12.3-13.1;
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Best Local
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Note: The sequence data for this patent did not form part specification, but was obtained in electronic format directions.
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                                                                                                                 Human; colon tumour;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATGATCCTGACAAGAAGAAAATGAAGCTCAAAGTCAAAAAATCTCGTGAAAAAACGGAGT
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                                                                                                                                                                                                                                                                                                                                                                                          TTGGCCTCTCATCTCAGTGGATATATCCCTCCCAAAAGGAAACAAGGGCAAGGCTTATCT
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                                                                                                                                                                  (first
                                                                                                                                          colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ence data for this patent did not form part of the printed but was obtained in electronic format directly from WIPO
                                                                                                   gene;
                                                                                                                                                                                                                      cDNA; 439
                                                                                                                                          tumour
                                                                                                                                                                  entry)
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94.8%;
                                                                                                     vaccine; colon ss.
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Pred. No. 2
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31-JUL-2001; 2001WO-US24218

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28-MAR-2001;
29-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The polynucleotides and encoded polypeptides are useful in pharmaceutical compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polynucleotide sequences may be used as hybridisation probes or primers, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating an immune response against cancer, particularly for the immunotherapy of colon cancer, and as markers for the progression of cancer.
                                                                                                                                             1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: With the exception of SEQ ID No 1 and 2, the sequence data for this patent did not form part of the printed specification but supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New colon cancer polypeptides and polynucleotides, useful as vaccines for diagnosing, preventing, and treating colon cancer, and as markers for the progression of cancer -
               ABK45138
                                            ABX45138 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK44450-ABK46237 represent coding sequences of human colon tumour proteins of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to polynucleotides encoding colon tumour proteins
                                                                                                               TCACCCAACTGTGTGGAAGACAAGATGCTCTCGACAGTTGCAGTACTTACCCTTGGCTAA
                                                                                                                                                                                        GGATATATCCCTCCCAAAAGGAAACAAGGGCAAGGCTTATCTTTGTGTCAAAACGGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                         CGCTGTCCAAGAGGAGGCTGTGGGAAGAACCTATACTGTGTGTTTAATCTCCAAAGCCAT 913
                                                                                                                                                                                                                                                  AAAATGAAGCTCAAAGTCAAAAAATCTCGTGAAAAAACGGAGTTTGGCCTCTCATCTCAGT 1093
                                                                                                                                                                                                                                                                                        CGCTGTCCAAGAGAAGGCTGTGGAAGAACCTATACAACTGTGTTTAATCTCCAAAGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002-241739/29
                                                                                                                                                                          GGATATATCCCTCCCAAAAGGAAACAAGGCCAAGGCTTATCTTTGTGTCAAAACGGAGAG
                                                                                                                                                                                                                                  AAAATGAAGCTCAAAGTCAAAAAATCTCGTGAAAAACGGAGTTTGGCCCTCATCTCAGT
                                                                                                                                                                                                                                                                                                                    ACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGATCCTGACAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID No 326; 147pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 2000US-223283P.
; 2001US-279763P.
; 2001US-302051P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      вP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.5%;
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Pred. No. 6.4e-102;
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28-MAR-2001;
29-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to polynucleotides encoding colon tumour proteins. The polynucleotides and encoded polypeptides are useful in pharmaceutica compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polynucleotide sequences may be used as hybridisation probes or primers, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating are
                                                                                                                                                                                                                                                                                                                                                        proteins of the invention.

Note: With the exception of SEQ ID No 1 and 2, the sequence dat for this patent did not form part of the printed specification supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                      immune response against cancer, particularly for the immunotherapy colon cancer, and as markers for the progression of cancer.

ABK44450-ABK46237 represent coding sequences of human colon tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                 1034
                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosing, preventing, and treating colon cancer, and as markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   colon cancer polypeptides and polynucleotides, useful as vaccines
                                                                                                                                                                                         CGCTGTCCAAGAGAAGGCTGTGGAAGAACCTATACTACTGTGTTTAATCTCCAAAGCCAT 913
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GGATATATCCCTCCCAAAAGGAAACAAGGGCAAGGCTTATCTTTGTGTCAAAAACGGAGAG
                                                AAAATGAAGCTCAAAGTCAAAAAATCTCGTGAAAAACGGAGTTTGGCCTCTCATCTCAGT 109
                                                                          ACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGATCCTGACAAGAAG
                                                                                     ACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGATCCTGACAAGAAG 1033
                                                                                                                          CGCTGTCCAAGAGAAGGCTGTGGAAGAACCTATACAACTGTGTTTAATCTCCAAAGCCAT 120
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                                                                                                                                                                                                                                                                                                                                  439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meagher
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                BP;
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2001US-279763P
2001US-302051P
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                                                                                                                                                                                                                                                                                                                                141 A; 99 C;
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                                                                                                                                                                                                                                                                                          Score 416.8; DB 24
Pred. No. 1.7e-101;
                                                                                                                                                                                                                                                                                                                                93 G; 106 T;
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Best I
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                                                                                                                                                                used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (1) is useful for detecting the presence or absence of a polynucleotide encoded by a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I), and for determining the phenotype of cells in a sample of cells from a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate corresponding gene resides, and in tissue profiling, forensics, genetic manufacture and disposations and in tissue profiling, forensics, genetic manufacture and disposations and in tissue profiling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1154
                                                                                                                                               antibodies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; colon cancer; cancer; tissue profiling; forensic; mapping;
genetic analysis; diagnostic; antisense therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ59499 standard;
                                                                                                                                                          analysis, mapping and diagnostic applications. (I) can be used to raise
                                                                                                                                                                                                                                                                                         expressed in cancer tissues. ABB78993 to ABB79004 represent proteins encoded by the ABG60776 to ABG60787 nucleic acid sequences. (I) can be
                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                           or tissue type, and in antisense therapy
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-426115/45
                                                                                                                                                                                                                                                                                                                                                                                                                              Thiaglingam
                                                                                                                                                                                                                                                                                                                                                                                                                                        Burgess C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-2000; 2000US-237271P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-OCT-2001; 2001WO-US30732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human colon
                                                                                                                        Sequence 537 BP; 196 A; 116 C; 106 G; 117 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid that is differentially expressed it tissues useful for determining the presence of colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200229086-A2
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             662
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                                                                                         Local Similarity
TCACCCAACTGTGTGGAAGACAAGATGCTCTCGACAGTTGCAGTACCTTACCCCTTGGCTAA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAAGGTCCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACAT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
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                                                       AAGTGTACCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACAT 661
                                                                                                                                                                                                                                                                                                                                       Fig 1; 796pp; English
                                                                                                                                                                                                                                                                                                               to ABQ60787 represent isolated nucleic acids (I) differentially
                                                                                                                                              and to screen for peptide analogues and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                        Astle JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer related nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              Lewis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA;
                                                                                       30.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Carroll E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  537
                                                                             0;
                                                                                      Score 374; DB 24;
Pred. No. 5.5e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Catino TJ,
                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Dwivedi P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID
                                                                                                 Length
                                                                             Indels
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n a cell
                                                                           Gaps
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-SEP-2002
                                                                                                                                                                                                                Schlegel
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a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of t specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                         Claim 1; Page 9624; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful
(d) assessing the efficacy of a therapy in a patient;(e) selecting a composition for inhibiti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-662795/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; prostate cancer; cytostatic; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostate expression marker cDNA 49222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABV49231 standard;
                                                                                                                                                                                                                                                    The invention relates to an
                                                                                                                                                                                                                                                                                                                                                                  for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PREDICTIVE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-FEB-2001; 2001WO-US05171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGGAACTTCTGAAACATGTGAGAGAAACCCCATAAAGAGGGAAATACTATGTGAAGTATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCTGTGGCAAAACATTTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCCAAAGCCATATCCTCTCCTTCCATGAGGAAAGCCCGCCTTTTTNGTGTGAACATGCT
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2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
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                                                                                                                                                                                                                   isolated nucleic acid molecule (I) comprising in Tables 1-9 (ABV00010-ABV62213) of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВР
  inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carcinogen; pharmacodyanamic marker;
                                                     for inhibiting prostate cancer
  prostate cancer in
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  patient,
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RESULT 12
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Best L
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                                                                                                                                     16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
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(g) dete:
(h) asse:
patient;
(I) is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, uses
                                                                                                                                                                                                                                                                                                                                                                       human; prostate cancer;
pharmacogenomic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABV19459 standard;
                                              WPI; 2001-662795/76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATGTGAGAGAAACCCATAAAGAGGAAATACTATGTGAAGTATGCCGGGAAAACATTTAAA
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                                                                                                         MILLENNIUM PREDICTIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               466
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2000US-211314P.
2000US-219007P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA;
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gene; ss.
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Pred. No. 1.4e-70;
0; Mismatches 1;
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) assessing the prostate cell carcinogenic potential of a compound;
(f) assessing the prostate cell carcinogenic potential of a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 425
                                                                                                                                                                                              Human eukaryotic initiation
                                                                                                                                                                                                                                      20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detecting presence of prostate cancer,
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                                                                                                   sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTCCAAGAGAAGGCTGTGGAAGAACCTATACTACTGTGTTTAATCTCCAAAGCCATATC
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                                                                                                                                        dendritic
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/product-
                                         Location/Qualifiers 237..1073
                                                                                                                                                                                                                                                                                                                  CDNA;
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99.7%;
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      "eukaryotic initiation
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                                                                                                                                                                                              factor 3 (heIF3) encoding cDNA
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Pred. No. 2.5e-70;
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23-AUG-2000; 2000US-0649167

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RESULT 14
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a human eukaryotic initiation factor (eIF), designated heIF3), which is expressed in human dendritic cells. heIF3 has translation initiation factor activity. Also described in the present invention are methods for the preparation and detection of the heIF3 protein and nucleotide sequences. The present sequence encodes heIF3, as given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human translation initiation factor protein and its
31-MAR-2000; 2000US-0540217
                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss
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                       30-MAR-2001; 2001WO-US08631
                                                    11-OCT-2001
                                                                                                                                                                        DNA encoding novel human diagnostic protein #9338
                                                                                                                                                                                                      13-FEB-2002
                                                                                                                                                                                                                                                          AAS73534 standard;
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                                                                              WO200175067-A2
                                                                                                        Homo sapiens
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les 246; Conserv
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                                                                                                                                                                                                                                                                                                                                                                              GGAGAGTCACCCAACTGTGGGAAGACAAGATGCTCTCGACAGTTGCAGTACTTACCCTT 1207
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100.0%; Pred. No.
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at figure in the printed specification, but was obtained in electronic format directly from WIPO at figure in the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 9338; 103pp; English
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               05-JUN-2002
                                                        ABK45059;
                                                                                              ABK45059 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1889 BP; 488 A; 453 C; 417 G; 531 T; 0 other;
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                                                                                                                                                                                                                                                                                                   CCCAAAAGGAAACAAGGGCAAGGCTTATCTTTGTGTCAAAACGGAGAGTCACCCAACTGT 1165
                                                                                                                                                                                                                                                                                                                                                             AAAGTCAAAAAATCTCGTGAAAAACGGAGTTTGGCCTCTCATCTCAGTGGATATATCCCT
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                                                                                                                                                                                                                                                                               CCCAAAAGGAAACAAGGCCAAGGCTTATCTTTGTGTCAAAAACGGAGAGTCACCCAACTGT
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               (first entry)
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95.5%;
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Pred. No. 9
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Search completed: February 10,
Job time : 293.158 secs
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ABK44450-ABK46337 represent coding sequences of human colon tumour cancer from the progression of cancer.
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28-MAR-2001; 2001US-279763P.
29-JUN-2001; 2001US-302051P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins of the invention.

Note: With the exception of SEQ ID No 1 and 2, the sequence data for this patent did not form part of the printed specification but was supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 610; 147pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New colon cancer polypeptides and polynucleotides, useful as vaccines for diagnosing, preventing, and treating colon cancer, and as markers for the progression of cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-241739/29
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                                                                                                                           GTGAGAGAACCCATAAAGAGGAAATACTATGTGAAGTATGCCGGAAAACATTT 234
                                                                                                                                                                                                GTGAGAGAAACCCATAAAGAGGAAATACTATGTGAAGTATGCCGGAAAACATTT 793
                                                                                                                                                                                                                                                                                                                                   TATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGGACGGAACTTCTGAAACAT 739
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sapien sapien

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Post-processing: Minimum Match 0%
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Z287_MOUSE
Z071_XENLA
Z228_HUMAN
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Z06_XENLA
Z226_HUMAN
ZN43_HUMAN
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                  Z189_HUMAN
Z155_HUMAN
ZG46_XENLA
ZF93_MOUSE
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ZN81_HUMAN
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RESULT 1
TF3A_HUMAN
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TISSUE-Fetal brain;
MEDLINE-95309028; PubMed-7789179;
Arakawa H., Nagase H., Hayashi N., Ogawa M., Nagata M.,
Arakawa T., Takahashi E., Shin S., Nakamura Y.;
Pujiwara T., Takahashi E., Shin S., Nakamura Y.;
"Molecular cloning, characterization, and chromosomal mapping novel human gene (GTF3A) that is highly homologous to Xenopus transcription factor IIIA.";
Cutomonet. Cell Genet. 70:235-238(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 269:20857-20865(1994).

-!- FUNCTION: INTERACTS WITH THE INTERNAL CONTROL REGION (ICR) OF APPROXIMATELY 50 BASES WITHIN THE 5S RNA GENES, IS REQUIRED FOR CORRECT TRANSCRIPTION OF THESE GENES BY RNA POLYMERASE III. ALSO BINDS THE TRANSCRIBED 5S RNA'S. MAY INITIATE TRANSCRIPTION OF THE 5S RIBOSOMAL RNA GENE AND MAINTAIN THE STABILITY OF TRANSCRIPTION OF OTHER GENES.

-!- TISSUE SPECIFICITY: UBIQUITOUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TF3A_HUMAN STANDARD; PRT; 423 AA. 092664; 013097; 012963; 01·NOV-1997 (Rel. 35, Created) 01·NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Transcription factor IIIA (Factor A) (TFIIIA).
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                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION.
MEDLINE-94342241; PubMed-8063702;
Moorefield B., Roeder R.G.;
"Purification and characterization of human
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus TFIIIA.";
Gene 159:215-218(1995).
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Becker K.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95347600; PubMed=7622052;
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RESULT 2
TF3A_XENLA
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Best Local :
Matches 36:
        TF3A_XENLA STANDARD; PRT; 366 AA. P03001; Q91856; 21-JUL-1986 (Rel. 01, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Transcription factor IIIA (Factor A) (TFIIIA)
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PROSITE; PS50157; ZINC_FINGER_C2H2_2; 8.
Transcription_regulation; Zinc-finger; metal-binding; DNA-binding;
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  "Multiple internal repeats within the strubinding transcription factor TF-IIIA from Studia Biophys. 107:237-247(1985).
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Amphibia; Batrachia;
Amphibia; Xenopus
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MEDLINE-91071597; PubMed-2253880;
Kim S.H., Darby M.K., Joho K.E., Brown D.D.;
"The characterization of the TFIITA synthesized
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                                                                                                                                         STRUCTURE BY NMR OF 10-101.
MEDLINE=97397344; PubMed=9253405;
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MEDLINE-85231235;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Taylor W., Jackson
"The developmental
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                                              MEDLINE-98169475; PubMed-9501194;
                                                                                            "Domain packing and dynamics zinc fingers of TFIIIA.";
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                                  Nolte R.T.,
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                        'Differing
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                                                                                                                                                                                                                                                        primary structure of transcription scutive repeats.";
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J. 4:1609-1614(1985).
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Conlin R.M., Harrison S.C., Brown R.S.; roles for zinc fingers in DNA recognition: transcription factor IIIA complex."; Acad. Sci. U.S.A. 95:2938-2943(1998).
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                                                                                                                                                                                                                                                 186:271-274(1985).
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PubMed=3754326;
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r C., Argos P.;
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an H., Roeder R.G.
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PROSITE; PS50157; ZINC_FINCER_C2H2_2; PS50157; ZINC_FINCER_C2H2_2; Perosite Property Metal-binding; Property Nuclear protein; Alternative initial RNA-binding; Repeat; Nuclear protein; Alternative initial RNA-binding; RNA-b
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L; X03736; CAB51745.1; JOINED.
L; X03737; CAB51745.1; JOINED.
L; X03738; CAB51745.1; JOINED.
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PTM: THE N-TERMINUS IS BLOCKED.
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; S-TFIIIA (IN SOMATIC CELLS) AND O-TFIIIA (IN OOCYTES); ARE PRODUCED BY ALTERNATIVE INITIATION.
TISSUE SPECIFICITY: SYNTHESIZED IN OOCYTES AND, IN MUCH LOWER LEVELS, IN SOMATIC CELLS.
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MAY PLAY AN ESSENTIAL ROLE IN THE DEVELOPMENTAL CHANGE IN 5S RNA GENE EXPRESSION. INTERACTS WITH THE INTERNAL CONTROL REGION (ICR)
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Gaskins C.J., Smith J.F., Ogilvie M.K., Hanas J.S.;
Gaskins C.J., Smith J.F., Ogilvie M.K., Hanas J.S.;
Caskins C.J., Smith J.F., Ogilvie M.K., Hanas J.S.;
Caskins C.J., Smith J.F., Ogilvie M.K., Hanas J.S.;
Consparison of the sequence and structure of transcription facto
IIIA from Bufo americanus and Rana pipiens.";
Gene 120:197-206(1992).
Cene 120:197-206(1992).
Cene 120:197-206(1992).
Cene 120:197-206(1992).
Cene 120:197-206(1992).
CONTROL REGION OF THESE GENES BY RNA POLYMERASE III.
BINDS THE TRANSCRIPTION OF THESE GENES BY RNA POLYMERASE III.
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p34695;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Transcription factor IIIA (Factor A) (TFIIIA)
                    Pfam; PF00096; zf-C2H2; 9. PRINTS; PR00048; ZINCFINGER. SMART; SM00355; ZNF_C2H2; 9.
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                                                                                                                                                                                                        EMBL; M85211; AAA49534.1;
EMBL; X58369; CAA41260.1;
                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rana pipiens (Northern leopard frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Ovary;
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                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDKKKMKLKVKKSREKRSLASHLSGYIPPKRKQGQGLSLCQNGESPNCVEDKMLST
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                                                                                      IPR000822; znf_C2H2
0096; zf-C2H2; 9.
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55.1%;
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Best Local
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01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Transcription factor IIIA (Factor A) (TFIIIA).
Xenopus borealis (Kenyan clawed frog).
                                         "A finger protein structurally similar exclusively to 5S RNA in Xenopus.";
                                                                                                                      MEDLINE-90245658; PubMed-2110661; Gaskins C.J., Hanas J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription
                                                           MEDLINE=90235278; PubMed=2331751;
Joho K.E., Darby M.K., Crawford E
                                                                                                  Gaskins C.J., Hanas J.S.;
"Sequence variation in transcription in
Nucleic Acids Res. 18:2117-2123(1990).
                                                                                                                                                                                Amphibla; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus.
                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                        TF3A_XENBO
                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                      NCBI_TaxID-8354;
                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                             YIHTNQQPFKCNHEGCDKSFSSPSRLKRHEKVHAGYPCQKDSSCSFVGKTWTEYMKHLAA 186
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C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
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Pred.
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C2H2-TYPE.
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C2H2-TYPE.
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ZINC FIN
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TFIIIA
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EEQRPFACEHAECGKSFAMKKSLERHSVVHDPEKR--KLKEKCPRPKRSLASRLSGCAPP EESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKKKKKLKVKKSREKRSLASHLSGYIPP CHOEPVMCDECKRTFKHKDYLRNHKKTHKKERTVYCCPRDGCERSYTTEFNLOSHMOSFH THKEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFH FTHTQQLPYKCPHEGCDKSFSVPSCLKRHEKVHAGYPCKKDDSCLFVGKTWTLYLKHVKE CQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQK--GCSFVAKTWTELLKHVRE HTGEKNFKCDSDKCDLTFTTKANMKKHFNRFHNLQLCVYVCHFEGCDKAFKKHNQLKVHQ HTGEKPFYCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00028; ZINC_FINGER_C2H2_1; EPROSITE; PS50157; ZINC_FINGER_C2H2_2; ETranscription regulation; Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0048; ZINCFINGER SMART; SM00355; ZnF_C2H2; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an
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                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00096; zf-C2H2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEVELS, IN SOMATIC CELLS.
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PVVYKRYICSFADCGASYNKNWKLRAHLCKHTGEKPFPCKEEGCDKGFTSLHHLTRHSIT
                                                                          PALPRREICSEPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P03001;
                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                        339
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                                                                                                                                                                                    Score 1024; DB Pred. No. 1.3e-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metal-binding; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OOCYTES AND,
                                                                                                                                                                                                                                                                                                                                             REET.
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                                                                                                                                                                                                                              DB 1;
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                                                                                                                                                    81;
                                                                                                                                                                                                                                                                                                        CRC64;
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InterPro; IPRUUU022, 9.
Pfam; PF00096; zf-C2H2; 9.
PRINTS; PR00048; ZINCTINGER_C2H2_1; 8.
SMART; SM00355; ZINC_FINGER_C2H2_1; 8.
PROSITE; PS00028; ZINC_FINGER_C2H2_2; 8.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Transcription factor IIIA (Factor A) (TFIIIA).
Bufo americanus (American toad),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                      ZN_FING
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                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; JC1442; JC1442.
HSSP; P03001; 1TF6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Comparison of the sequence and structure of transcription fact
IIIA from Bufo americanus and Rana pipiens.";
Gene 120:197-206(1992).
-i- FUNCTION: INTERACTS WITH THE INTERNAL CONTROL REGION (ICR)
APPROXIMATELY 50 BASES WITHIN THE 5S RNA GENES, IS REQUIRED
CORRECT TRANSCRIPTION OF THESE GENES BY RNA POLYMERASE III.
BINDS THE TRANSCRIBED 5S RNA'S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P34694;
                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X58366; CAA41259.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93013035; PubMed-1398134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-8389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TF3A_BUFAM
                                                                                                                                                                                                                                                                                                 ZN_FING
154 CQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQKG--CSFVAKTWTELLKHVRE 211
                          66
                                                  94
                                                                                       34 PALPRREICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILT 93
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                       HTGEKPCKCETENCNLAFTTASNMRLHFKRAHSSPAQVYVCYFADCGQQFRKHNQLKIHQ
                                       HTGEKPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQ 153
                                                                           PVVYKRFICSFPDCNATYNKNRKLQAHLCKHTGERPFPCTYEGCEKGFVTLHHLNRHVLS
                                                                                                                             189;
                                                                                                                                           Similarity
                                                                                                                                                                             : Repeat;
12 27
12 27
12 37
42 6
72 5
104 1;
134 1;
136 1
161 1
161 1
190 2
219 2
250 2
                                                                                                                               Conservative
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C2H2-TYPE.
                                                                                                                                      Score 1022; DB 1,
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                                                                                                                                                                               24CE3252696183CB CRC64;
                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA GENES, IS REQUIRED BY RNA POLYMERASE III.
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                                                                                                                                                      DB 1;
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                                                                                                                             97;
                                                                                                                                                    Length 339;
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TF3A_ICTPU
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P79797;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Transcription factor IIIA (Factor A) (TFIIIA)
                                                                                                                                                                    PRIMTS, PRO0048; ZINCFINGER.
SMART; SM00355; ZOF_CZH2; 9.
PROSITE; PS00028; ZINC_FINGER_CZH2_1; 8.
PROSITE; PS50157; ZINC_FINGER_CZH2_2; 8.
                                                                                                                                 DOMAIN
                                                                                                                                              RNA-binding;
                                                                                                                                                             Transcription
                                                                                                                                                                                                                             InterPro; IPR000822; znf_C2H2.
Pfam; PF00096; zf-C2H2; 9.
                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and characterization of TFIIIA from channel Gene 203:103-112(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ogilvie M.K., Hanas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98086209; PubMed-9426240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
                                                                                                                                                                                                                                                       HSSP; P03001;
                                                                                                                                                                                                                                                                   EMBL; 268499;
                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular biology of vertebrate transcription factor IIIA: and characterization of TFIIIA from channel catfish oocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ictalurus punctatus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302
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                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: INTERACTS WITH THE INTERNAL CONTROL REGION (ICR) APPROXIMATELY 50 BASES WITHIN THE 5S RNA GENES, IS REQUIRED CORRECT TRANSCRIPTION OF THESE GENES BY RNA POLYMERASE III. BINDS THE TRANSCRIBED 5S RNA'S (BY SIMILARITY).
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSKKKKKPSQTPAMESQEQQPDASKADPLPVLENLTL 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---PKRKQGQGLSLCQNGESPNCVEDKMLSTVAVLTL 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENLRPFVCEHEGCGKTFAMKQSLDRHFNTHDPEKKKM---VKPPRPVRSLASRLSGYKPK
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                                    Repeat;
12 27
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132 1:
188 2:
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                                                                                                                                                           regulation;
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                                                                                                                                                          Zinc-finger; Metal-binding; DNA-binding;
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EC30CE6E858F8456 CRC64;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDILINE-90235278: PubMed-2331751;
Joho K.E., Darby M.C., Crawford E.T., Brown D.D.;
Joho K.E., Darby M.C., Crawford E.T., Brown D.D.;
"A finger protein structurally similar to TFIIIA that binds exclusively to 5S RNA in Xenopus.";
cell 61:293-300(1990)
-1-FUNCTION: P43 IS A 5S RNA BINDING PROTEIN WHICH IS A MA.
CONSTITUENT OF OCCYTES AND COMPRISES PART OF A 42S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
P43 55 RNA binding protein (425 P43) (Thesaurin
Pfam: PF00096; zf-C2H2; 9.
PRINTS; PR00048; ZINCFINGER.
SMARF; SM00355; ZnE_C2H2; 9.
PROSITE; PS00028; ZINC_FINGER_C2H2_1;
                                                                                                                                          EMBL; M32473; AAA49714.1; -. PIR; C34895; C34895. HSSP; P03001; ITF3.
                                                                                                                                                                                                                                                                                                                            modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: I
Amphibia: Batrachia: Anura: Mesobatrachia: Pipoidea:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P43_XENLA
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                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BINDING PROTEIN 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIBONUCLEOPROTEIN STORAGE PARTICLE.
SUBUNIT: THE 42S RNP PARTICLE COMPRISES FOUR SUBUNITS EACH OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TWO MOLECULES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WHICH CONTAINS ONE MOLECULE OF 5S RNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDDSELPAQLHGLSL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----QGQGLSL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFICPHDGCGKAFAMEGSLKRHAVVHDPQKKKLQKKTKRGRKKK------LEPKTNV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFVCEHAGCGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKSREKRSLASHLSGYIPPKRK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVC-QKGCSFVAKTWTELLKHVRETHKEE 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHT 157
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                                                                                                                                                                                                                                                              requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                      and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                  non-profit institutions as long
                                                                                                                IPR000822; Znf_C2H2
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Pred. No. 1.1e-55;
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P25066;
                                                                                                                                                               Joho K.E., Darby M.K., Crawford E.T., Brown D.D.;
A finger protein structurally similar to TFIIIA that binds
exclusively to 55 RNA in Xenopus.";
Cell 61:293-300(1990).
-I- FUNCTION: P43 IS A 55 RNA BINDING PROTEIN WHICH IS A MA.
CONSTITUENT OF OCCYTES AND COMPRISES PART OF A 42S
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         the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Famphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                     P43 5S RNA binding protein (42S P43) (Thesaurin
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                                                                                                                                                                                                                                                       MEDLINE=90235278; PubMed=2331751;
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8354;
                                                                                                                                                                                                                                                                                                              Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                         Xenopus borealis (Kenyan clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195
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                                                                                                         SUBUNIT: THE 42S RNP PARTICLE COMPRISES FOUR SUBUNITS EACH OF WHICH CONTAINS ONE MOLECULE OF 5S RNA, THREE MOLECULES OF TRNA, TWO MOLECULES OF P50 (EFI-ALPHA) AND ONE MOLECULE OF THE 5S RNA
                                                                                               BINDING PROTEIN 43.
                                                                                                                                                      RIBONUCLEOPROTEIN STORAGE PARTICLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FKCTQEGCGKHFASPSKLKRHAKAHEGYVCQ-KGCSFVAKTWTELLKHVRETHKEEILCE 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCE
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                                                  SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSGCTRSFAMRESLLRHLVVHDPERKKLKLKFVRGPSK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVCDVPGCSWKSSSVAKLVAHQKRHRGYRCSYEGCQTVSPTWTALQTHVKK-HPLELQCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2EB5BE66D7192995 CRC64;
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01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Zinc finger x-linked protein ZXDB.
       MEDLINE-94093547; PubMed-8268913; Greig G.M., Sharp C.B., Carrel L., Willard H.F.; Toppilcated zinc finger protein genes on the proximal short the human X chromosome: isolation, characterization and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0048; ZINCFINGER.
SMART; SM00355; ZNF_C2H2; 9.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 7.
Zinc_finger; Metal-binding; RNA_binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M32471; AAA49712.1; PIR; A34895; A34895.
                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
X-inactivation studies.";
                                                        TISSUE-Brain;
                                                                SEQUENCE
                                                                                     Submitted (MAR-1999) to
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                 ZXDB_HUMAN
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                                                                                                                                 NCBI_TaxID=9606;
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rPro; IPR000822; Znf_C2H2
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                                                                                                                                                                                                                                                                                                                                                 KK-HPLELQCAACKKPFKKASALRRHKATHAKNPLQLPCPRQDCDKIFSTVFNLTHHLRK
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                                                                OF 307-709
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D7E8C76E80E42EF2 CRC64;
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                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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SMART; SM00355; ZnF_C2H2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z99130; CAB16205.1;
EMBL; L14788; AAC37522.1;
HSSP; P03001; 1TF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL031115; CAB36858.1; -. EMBL; Z99130; CAB16205.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
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PROSITE; PS50157; ZINC_FINGER_C2H2_2;
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561
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KHSMKTHM----VKRHKVGQDL
                       KRSLASHLSGYIPPKRKQGQGL 339
                                                                     QSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVVH---DPDKKKMKLKV----KKSRE
                                                                                                KLLRH
                                                                                                                 ELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNL
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                                               KGHSIT-HLGTKPFVCPVAGCCARFSARSSLYIHSKKHLQDVDTWKSRCPISSCNKLFTS
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ZINC FINGERS.
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ZN_FING 145
ZN_FING 155
ZN_FING 199
ZN_FING 222
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Submitted
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                                                                                  PROSITE; PS50805; KRAB; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1;
PROSITE; PS50157; ZINC_FINGER_C2H2_2;
                                                                                                                 PRINTS; PRO00048; ZINCFINGER.
PRODOMO 3; Znf_C2H2; 7
SMART; SM00349; KRAB; 1
SMART; SM00355; ZnF_C2H2; 16.
                                                                                                                                                                                                                      EMBL; M61873; AAA83548.1; -. PIR; H39384; H39384. H5SP; P08046; TA1H.
                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                        "The evolutionarily conserved Kruppel-associated box domain subfamily of eukaryotic multifingered proteins.", Proc. Natl. Acad. Sci. U.S.A. 88:3608-3612(1991).
-I- FUNCTION. MAY BE INVOLVED IN TRANSCRIPTIONAL REGULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-191 FROM N.A. MEDLINE-91219421; PubMed-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carrano A.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Andreise T., Trankhelm M., Amico-Keller G., Coefield J., Duarte S.,
Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,
Sanders C., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, L
16-OCT-2001 (Rel. 40, L
16-OCT-2001 protein 93
                                                                                                                                                          Pfam; PF00096; zf-C2H2; 16.
Pfam; PF01352; KRAB; 1.
                                                                                                                                                                              InterPro; IPR001909; KRAB.
InterPro; IPR000822; Znf_C2H2
                                                                                                                                                                                                    MIM; 603975; -
                                                                                                                                                                                                                                                      EMBL; AC007204; AAD22981.1; -.
                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                            between
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91219421: PubMed=2023909;
Bellefroid E.J., Poncelet D.A., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                             Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Martial J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence analysis of a 5.7 Mb region in 19p13.1 between D19s455.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 1 KRAB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear (Probable).

DEVELOPMENTAL STAGE: EXPRESSED EARLY DURING EMBRYONIC DEVELOPMENT SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                    FINGER PROTEINS
                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                            HGNC:13169; ZNF93.
                                                               procein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (APR-1999) to
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41
141
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225
                                                                         regulation; Zinc-finger;
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                                                               Kepeat.
   71
163
191
219
247
                                                                                                                                                                                                                                                                                  tatement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
3 (Zinc finger protein HTF34) (Fragment).
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                                                                         DNA-binding; Metal-binding;
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                      PIR; S06578; S06578.
HSSP; P25490; 1ZNM.
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                                                                                                                             Xenopodinae;
                                                                                                                  NCBI_TaxID - 8355;
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              interPro;
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  PF00096; zf-C2H2;
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              IPR000822;
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SEQUENCE FROM N.A.
MEDLING-90040698; PubMed-2509712;
Nietfeld W., El-Baradi T., Mentze
Poeting A., Knoechel W.;
"Second-order repeats in Xenopus
J. Mol. Biol. 208:639-659(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last Sequence update)
01-FBB-1994 (Rel. 28, Last annotation update)
Gastrula zinc finger protein XLCGF57.1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 YICE--ECGKAFKYSSALNTHKRIHTGEKPYKCD--KCDKAFIASSTLSKHEIIHTGKKP 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CEECGKAFI---WSSVLTRHKRVHTGEKPYKCEECGKAFKYSSTLSSHKRSHTGEKPY-K
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Znf_C2H2
2H2; 12.
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                                                                                                                                                                                                                                                                                                               T., Mentzel H.,
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SM00355; ZnF\_C2H2; 12

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RAPPARATE RAPACTOR REPRESENTATION OF THE PROPERTY OF THE PROPE
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PROSITE; PS00
Zinc-finger;
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ZN_FING
ZN_FI
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01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Zinc finger X-linked protein ZXDA.
                   MEDLINE-94093547; PubMed-9268913;
Greig G.M., Sharp C.B., Carrel L., Willard H.F.;
"Duplicated zinc finger protein genes on the proximal short
the human X chromosome: isolation, characterization and
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Bird C.;
X-inactivation studies.";
                                                                                                                                                          TISSUE-Brain
                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                         Submitted (JUN-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZXDA_HUMAN
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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PS50157; ZINC_FINGER_C2H2_2; 12.
ger; Metal-binding; DNA-binding; Repeat.
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Pred. No. 1
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-!- SUBCELLULAR LOCATION: Nuclear (
-!- TISSUE SPECIFICITY: UBIQUITOUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL034396; CAB46717.1; -. EMBL; L14787; AAC37521.1; -. HSSP; P03001; 1TF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SMART; SM00355; ZnF_C2H2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000822; Znf_C2
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                                                                 LKV----KKSREKRSLASHLSGYIPPKRKQGQGL
                                                                                       GCGKSFTRAEHLKGHSIT-HLGTKPFVCPVAGCCARFSARSSLYIHSKKHLQDVDTWKSR
                                                                                                   FDGCGWNFTSMSKLLRH
                                                                                                                                                          -KGCSFVAKTWTELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPRE
                                                                                                                                                                                 SGCKKTFITVSALFSHNRAHFREQELFSCSFPGCSKQYDKACRLKIHLRSHTGERPFLCD
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ZINC FINGERS.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                              Score 409;
Pred. No. 4
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Transcription
Nuclear protein
DOMAIN
DOMAIN
9
                                                                                                    SMART: SMOUJDJ, ....AB; 1.

PROSITE; PS50805; KRAB; 1.

PROSITE; PS50128; ZINC_FINGER_C2H2_1; 1

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1

PROSITE; PS50157; DNA-binding;
DOMAIN
ZN_FING
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ZN_FING
ZN_FING
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EMBL; X78927; CAA5527.1; -.
EMBL; AC074331; AAF88104.1; -.
HSSP; P08047; 1SP2.
Genew; HGNC:13027; ZNF234.
                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kodoylanni V., Ge Y., Severin J., Krummel G.K., Grable L., Kvikstad E., Gordon L., Shannon M., Brower A., Olsen A.S., "Sequence analysis of a 1Mb region in 19q13.2 containing a gene cluster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Isolation of cDNA ciones for 42 different Kruppel-related zinc proteins expressed in the human monoblast cell line U-937."; DNA Cell Biol. 14:125-136(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                        PRINTS: PRODOAB: ZINCFINGER.
PRODOMOOS: ZNÍ_C2H2; 5
SMART: SMOO349; KRAB; 1.
SMART: SMOO355; ZNF_C2H2; 19.
                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Differential expansion of homologous zinc-finger gene families human chromosome 19q13.2 and mouse chromosome 7."; submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
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zwr234 OR ZWF269.
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Q14588; Q9
                                                                                                                                                                                                        Pfam; PF00096; zf-C2H2; 19.
Pfam; PF01352; KRAB; 1
                                                                                                                                                                                                                                                          MIM; 604750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 7-698 FROM N.A.
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                                                                                                                                                                                                                                 InterPro; IPR000822;
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15-JUN-2002 (Rel. 41, Last sequence up
                                                                                                                                                                                                                                           InterPro; IPR001909; KRAB
                                                                                                                                                                                                                                                                                                                                                                             by non-profit institutions as long
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ZINC TYPE.
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C2H2-TYPE.
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                                                                                                          Zinc-finger; Metal-binding;
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ZN41_HUMAN
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CONFLICT
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                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                           SEQUENCE FROM N.A., MEDLINE-99380103; Pt
                                                                                                                                                                                                 ZNF41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                Cytogenet.
                                                           X-chromosome inactivation finger gene_ZNF41.";
                                                                       Rosati M., Franze A., Matarazzo M.R., Grimaldi G.; "Coding region intron/exon organization, alternative splicing and X-chromosome inactivation of the KRAB/FPB-domain-containing human
                                                                                                                                                                                    Homo sapiens (Human)
 Franze A.,
             MEDLINE=91244317;
                         SEQUENCE OF 280-821 FROM N.A.
                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                              522
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                                                                                                                                                                                                                                                                                                                                                                                                                                             GKSFRMKIHYQVHLVVHTGEKPYKCEVCGKAFRQSSYLKIHLKAHSVQKPF-KC--EECG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -CGKNFRRRSALNNHC--MVHTGEKPYKC--EDCGKCFTCSSNLRIHQRVHTGEKPYKC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - ECGKGFSRRSTLTVHCKLHSGEKPYNC--EECGRAFIHASHLQEHQRIHTGEKPFKCDT-
                                                                                                                                                                                                                                                                                                                                                                      AMKQSLTRHAVVHDPDKKKMKLKVKKSREKRSLASHLSGY 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QEGCGKHFASPSKLKRHAKAHEG---YVCQ---KG-----
                                                                                                                                                                                                                                                                                                                                              SQASHLLTHQRVHSGEK---PFKCEECGKSFSRSAHLQAH 558
                                                                                                                                                                                                                                                                                                                                                                                            QGFNQSSRLQIHQL-IHTGEKPYKCEECGKGFNRRADLKIHCRIHTGEKPYNCEECGKVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -EECGKCFIQPSQFQAHRRIHTGEKPYVCKVCGKGFIYSSSFQAHQGVHTGEKPYKCNEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
 Archidiacono N., Rocchi M.,
                                                  Cell
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                                                  Genet.
                                                                                                           ., AND ALTERNATIVE SPLICING Pubmed=10449920;
             PubMed-2037297;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.2%;
                                                                                                                                                                                                                      Last annotation update
                                                  85:291-296(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 406; DB 1;
Pred. No. 6.5e-24
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                                                                                                                                                                                                                                                                     Q9UMV6; Q9UMV7; Q9UMV8; Q9UMV9;
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  Marino
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Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
             VARSPLIC
                                                                                                                                                                                                                                                                                                                    SMART; SM00349; KRAB; 1.
SMART; SM00355; ZnF_C2H2; 17.
PROSITE; PS50805; KRAB; 1.
                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00096; zf-C2H2; Pfam; PF01352; KRAB; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 142-821 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Isolation and expression analysis of a human zinc finger gene (ZNF41) located on the short arm of the X chromosome.";
                                                                                                                                                                                                                                                                                        Transcription
                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000003; Znf_C2H2; 14
                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000822;
                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001909; KRAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FINGER PROTEINS.
SIMILARITY: CONTAINS 1 KRAB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear (Potential).
ALTERNATIVE PRODUCTS: At least 8 isoforms; 1 (shown here), 2, 4, 5, 6, 7 and 8; are produced by alternative splicing.
SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                   L; X60155; CAB51740.1; -
L; AJ010017; CAB53035.1; -
L; AJ010018; CAB53037.1; -
L; AJ010019; CAB53037.1; -
L; AJ010020; CAB53038.1; -
L; AJ010022; CAB53039.1; -
L; AJ010022; CAB53000.1; -
L; AJ010023; CAB5304.1; -
L; AJ010023; CAB5304.1; -
L; AJ010023; CAB5304.1; -
L; AJ010023; CAB5304.1; -
L; MJ02443; AAA66312.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: MAY BE
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P25490; 12
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HGNC:13107; ZNF41.
                                                                                                                                                                                                                                                                                                PS00028; ZINC_FINGER_C2H2_1; 17
PS50157; ZINC_FINGER_C2H2_2; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             located on the sh
9:728-736(1991).
                                                                                                                                                                                                                                                                                     regulation; DNA-binding; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                            CAC88162.1;
                                                                                                                                                                                                                                                                           Repeat; Alternative splicing.
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7; 51
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                                                                                                                                                                                                                                                                                                                                                                                        C2H2
                                                      C2H2-TYPE.
                                                                                                                                                                          C2H2-TYPE.
                                                                                                                                                                                                C2H2-TYPE.
                     PDLSPGPKGRSSADHAALN -> MGTLPHGPRPWLQRDVAA
HV (IN ISOFORM 7 AND ISOFORM 2).
                                           MAANGDSPPWSPALAAEGRGSSCEVRRERTPEARIHSVKRY
           MAANGDSPPWSPALAAEGRGSSCEVRRERTPEARTHSVKRY
                                                                                                                                                                                                                                 (DEGENERATE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                  "Prediction of the coding sequences The complete sequences of 100 new cl for large proteins in vitro."; DNA Res. 7:143-150(2000).
                                                                                                                                                                                                                                                                                                                                                                              Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.; "Prediction of the coding sequences of unidentified human genes." The complete sequences of 100 new cDNA clones from brain which complete sequences of 100 new cDNA clones from brain which complete sequences of 100 new cDNA clones from brain which complete sequences of 100 new cDNA clones from brain which complete sequences of 100 new cDNA clones from brain which complete sequences of 100 new cDNA clones from brain which complete sequences of 100 new cDNA clones from brain which complete sequences of 100 new cDNA clones from brain which complete sequences of 100 new cDNA clones from brain which complete sequences of 100 new cDNA clones from brain which complete sequences of 100 new cDNA clones from brain which complete sequences of 100 new cDNA clones from brain which complete sequences of 100 new cDNA clones from brain which complete sequences of 100 new cDNA clones from brain which complete sequences of 100 new cDNA clones from brain which complete sequences of 100 new cDNA clones from brain which complete sequences of 100 new cDNA clones from brain which complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the clones from the clones complete sequences of 100 new cDNA clones from the clones from the clones complete sequences of 100 new cDNA clones from the clones 
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15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42
                                                                                                                                                                                                                                                         FUNCTION: MAY FUNCTION AS A TRANSCRI
SUBCELLULAR LOCATION: Nuclear (Proba
SIMILARITY: BELONGS TO THE KRUEPPEL
                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 KRAB DOMAIN.
                                                                                                                                                                                                                                    FINGER PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CS--DCGKSFTKKSQLHVHQRIHTGEKPYIC--TECGKVFTHRTNLTTHQKTHTGEKPYM 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TECOKAFTDRSNLIKHOKMHSGEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKVKKSREKRS-LASHLSGYIPPKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYECGDCGKTFTWKSRLNIHQKSHTGERHYECSKCGKAFIQKATLSMHQIIHTGKKPYAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFVC-----EHAG-----CGKTFAMKQSLTRHAVVHDPDKKKMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YECSDCGKCFTKKSQLRVHQKIHTGEKPNIC----AECGKAFTDRSNLITH-QKIHTREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILCEVCRKTFKRKDYLKQHMKTHAPER-DVCRCPREGCGRTYTTVFNLQSHILSFHEESR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEC--KDCGKAFIQKSTLSVHQRIHTGEKPYVCPECGKAFIQK--SHFIAHHRIHTGEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQK-GCSFVAKTWTELLKHVR-ETHKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAE--CGKAFTDQSNLIKH--QKTHTGEKPYKCN--GCGKAFIWKSRLKIHQKSHIGERH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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41, Last sequence update)
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finger protein KIAA1473 (Fragment).
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MISSING (IN ISOFORM MISSING (IN REF. 1); C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.16
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 404; DB 1;
Pred. No. 1.1e-23;
                                                                                                                                                                                                                                                                                   A TRANSCRIPTION lear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      816
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'808C9A8AF13 CRC64;
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(IN ISOFORM 7 AND ISOFORM
                                                                                                          There are no
                                                                                                                                                                                                                                                              FAMILY OF C2H2-TYPE ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae; Homo.
                                                                                                                                                                                                                                                                                                             FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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5).
                                                                                                               he EMBL outstation restrictions on in
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                                                                                                                                            collaboration -
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Prodom; PD000003; ZRAB; 1.
SMART; SM00349; KRAB; 1.
SMART; SM00355; ZNE_C2H2; 13.
PROSITE; PS00028; KRAB; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 12.
PROSITE; PS00028; ZINC_FINGER_C2H2_2; 13.
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Pfam; PF00096; zf-C2H2; 13.
Pfam; PF01352; KRAB; 1.
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                                                                                                                                                                                                                                                                                                                         216 ECGKAYNETSNLSTHKRIHTGKKPYKC--EECGKAFNRLSHLTTHKIIHTGKKPYKCEE- 272
                                                                               312 VKKSREKRSLASHLSGYIPPKRKQGQGLSLCQNGESP-NCVE 352
                                                                                                                                                                                                                                                                                                                                                      46
                                                                                                                                                                                                                                                                                      YEECGKAFNQSSHLTTH-----KMIHTGEKPYKCEE
                                                                                                                                                                                                                                 CKKTFKKHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQKGC 195
                                                                                                                                                                                                                                                                                                                                                     DCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAAT 105
                                                                                                                                   RTYTTVFNLQSHILS---FHEESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKKKMKLK 311
                                                                                                                                                              GKAFKQSSTLTTHKRIHAGEKFYKCEVCSKAFSRFSHLTTHKRIHTGEKPY-KC--EECG 442
                                                                                                                                                                            SFVAKTWTELLKHVRETHKEEIL-CEVCRKTFKRKDYLKOHMKTHAPERDVCRCPREGCG 254
                                                                                                                                                                                                                 CGKAFSQSSTLTTHKIIHTGEKFYKC -- EECGKAFSQLSHLTTHKRIHSGEKPYKCEE - C 385
                                                                                                                                                                                                                                                                         -CGKAFNQSANLTTH-KRIHTGEKPYKCEECGRAFSQSSTLTAHKIIHAGEKPYKC--EE 328
                                                                                                         K----AFNLSSQLTTHKIIHTGEKPYKCEE--CGKAFNQSSTLSKHKVIHTGEK---PYK 493
                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; Transcription regulation; DNA-binding;
Metal-binding; Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                              20.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       65951 MW;
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                                                                                                                                                                                                                                                                                                                                                                               %; Score 403; DB 1; Length 574;%; Pred. No. 8.9e-24;47; Mismatches 121; Indels 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                    C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE (DEGENERATE).
C2H2-TYPE.
C2H2-TYPE.
482E5F1176ECA5B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRAB.
ZINC FINGERS.
C2H2-TYPE.
                                                      524
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Minimum DB seq
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    No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

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1213
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US-09-422-385-1
US-09-422-385-1
US-09-422-385-1
US-09-362-123A-3
US-09-362-123A-3
US-09-657-0227A-1
US-08-523-463-1-1
US-08-99-657-042A-3
US-08-946-241B-1
US-08-946-241B-1
US-08-946-241B-1
US-08-946-241B-1
US-08-99-053-1
US-08-946-241B-1
US-08-946-241B-1
US-08-946-241B-1
US-08-99-053-1
US-09-309-053-1
US-09-309-053-1
US-09-309-053-1
US-09-37-179B-1
US-08-317-179B-3
US-08-244-783-3
US-08-244-783-3
US-08-247-7522A-3
US-08-317-522A-8
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Result

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## ALIGNMENTS

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FILING DATE:
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEFAX: 6491103
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1399 base pairs
                                                   ; NAME/KEY: CDS
; LOCATION: 20..1288
; IDENTIFICATION METHOD:
US-08-523-376-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application Patent No. 5808030 GENERAL INFORMATION:
Query Match
Best Local Similarity
                                                                                                                        IMMEDIATE SOURCE:
LIBRARY: human
CLONE: OTK7
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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ADDRESSEE: Sughrue, Mion, Zinn, M.
STREET: 2100 Pennsylvania Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sadahito, SIN TITLE OF INVENTION: hTFIIIA GENE NUMBER OF SEQUENCES: 8
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APPLICANT:
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                                                                                                                                                                                             TOPOLOGY: 1:
MOLECULE TYPE:
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CITY: Washington
STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yoshikazu, SHIMADA
Kouichi, OZAKI
                                                                                                                                                           human fetal brain cDNA
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Satoshi, TAKEDA
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99.3%;
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Score 1170; DB 1;
Pred. No. 2.1e-303;
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             TCCTGACAAGAAGAAATGAAGCTCAAAGTCAAAAAATCTCGTGAAAAAAC-GGAGTTTGG
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                                                          TGGCTGTGGCAAAACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGA
                                                                                                        ACGCAAACATGAAAATCAACAAAAACAATATATATGCAGTTTTGAAGAGTGTAAGAAGAC
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TCCTGACAAGAAGAAATGAAGCTCAAAGTCAAAAATCTCGTGAAAAACGGGAGTTTGG
                                            TGGCTGTGGCAAAACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGA
                                                                                            CTTTAAGAAACATCAGCAGCTGAAAATCCATCAGTGCCAGCATACCAATGAACCTCTATT
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RESULT 2
US-08-52-376-1
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TITLE OF IN
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CORRESPONDE
ADDRESSEE
STREET
COUNTRY:
ZIP: GITY: WA
STATE: I
COUNTER NA
COMPUTER NA
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COUNTRY: WA
STATE: I
COMPUTER NA
SOFTWARE:
CURRENT APPLICANT
FILING DA
TELEFOMMUNI
TELEFAX:
TELEX: I
SEQUENCE CI
LENGTH: NI
SEQUENCE
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SEQUENCE
TYPE: DI
                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: cDNA US-08-523-376-1
                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.3
..... 1203; Conservative
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202) 293-786
TELEFAX: (202) 293-786
TELEX: 6491103
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/523,376
FILING DATE:
CLASSIFICATION: IFORMATION:
TELECATION INFORMATION:
TELECATION: (202) 293-7860
TELECATION: (202) 293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: YOShikazu, SHIMADA
APPLICANT: Kouichi, OZAKI
APPLICANT: Sadahito, SIN
TITLE OF INVENTION: hTFIIIA GENE
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                 181
                                                180
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                                                                                                              120
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STREET: 2100 Pennsylvania Avenue,
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
                                                                                                                                                                                                                                                                                                                                    LENGTH: 1269 base pai
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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TCCGCCGGCCGTGGTCGCCGAGTCGGTGTCGTCGTTGACCATCGCCGACGCGTTCATTGC
                                                                                                                                                                          GTGCCGGCGCGCGAAGGTTCAGCAGGGAGCCGTGGGCCGGGCGGCGGCTTCCCGGC
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                                                                                                                            ACGTGTCTCGGCACGTGGCAGCGCGCCTGGCCCTGGGCTTGGAGGCGCCGGGCGCCCTGGA 120
                                                TCCGCCGGCCGTGGTCGCCGAGTCGGTGTCGTCCTTGACCATCGCCGACGCGTTCATTGC
                                                                                                          ACGTGTCTCGGCACGTGGCAGCGCGCCTGGCCCTGGGCTTGGAGGCGCCGGCGCCCTGGA 179
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99.3%;
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Pred. No. 1.3e-302;
0; Mismatches 5;
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RESULT 3
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                                                                                                                                                                                                                                                                                      TGGCTGTGGCAAAACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGA
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                                                                                                                             GTCAAAACGGAGAGTCACCCAACTGTGTGGAAGACAAGATGCTCTCGACAGTTGCAGTAC
                                                                                                                                                                       CCTCTCATCTCAGTGGATATAT-CCTCCCAAAGGAAACAAGGGCAAGGCTTATCTTTGT
                                                                                                                                                                                                                              CCGGAAAACATTTAAACGCAAAGATTACCTTAAGCAACACATGAAAACTCATGCCCCCAGA
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                                                                                                                GTCAAAACGGAGAGTCACCCAACTGTGTGGAAGACAAGATGCTCTCGACAGTTGCAGTAC
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; LENGTH: 1471
; TYPE: DNA
; ORGANISM: mouse
US-09-492-985-11
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APPLICANT: Chen, Ya.Fen
APPLICANT: Chen, Ya.Fen
APPLICANT: KIENSKY, Alan M.
TITLE OF INVENTION: RFLAT-1: A Transcription Factor That
TITLE OF INVENTION: ACLIVATES RANTES Gene Expression
FILE REFERENCE: SUN-113P
CURRENT APPLICATION NUMBER: US/09/492,985
CURRENT APPLICATION NUMBER: US/09/492,985
CURRENT APPLICATION NUMBER: 05/117,576
EARLIER APPLICATION NUMBER: 05/117,576
EARLIER APPLICATION ONES: 11
NUMBER OF SEQ ID NOS: 11
CORMINER: FILING DATE: 1999-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-09-492-985-1
                                                                                                                          NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
                                                                                                                                                                                         APPLICANT: Song, An M.
APPLICANT: Krensky, Alan M.
APPLICANT: Krensky, Alan M.
TITLE OF INVENTION: RELAT-1: A Transcription Factor That
TITLE OF INVENTION: Activates RANTES Gene Expression
FILE REFERENCE: SUN-113P
CURRENT APPLICATION NUMBER: US/09/492,985
CURRENT FILING DATE: 2000-01-27
EARLIER APPLICATION NUMBER: 60/117,576
EARLIER FILING DATE: 1999-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application Patent No. 6376240
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Best Local Similarity 48.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version SEQ ID NO 11
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                           ORGANISM: homo sapien FEATURE:
                                                                               TYPE: DNA
OTHER INFORMATION: synthetic oligonucleatide probe
                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1015 GGACGAGCTGGCACGGCACTATCGCACGCACACGGGCGAGAAGAAGTT 1062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCGGCGAGGCCGGAGCCGCGCGCGCAGTCCCCGCAGAGGAAGCACAAGTGCCACTA 894
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; LOCATION: (82)..(1710)
US-09-362-123A-3
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                                                                                                                                          Query Match
Best Local Similarity
Matches 142; Conserv
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SOFTWARE: PatentIn V
SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Holness, Claire
APPLICANT: Sirenko, Oksana
TITLE OF INVENTION: No. 6451558el Genes in
FILE REFERENCE: 4-30629A/SYS
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/362,123A CURRENT FILING DATE: 1999-07-27 PRIOR APPLICATION NUMBER: 09/128,310 PRIOR FILING DATE: 1998-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cooke, Michael Paul
                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                          LENGTH: 2992
1323
                                                                       1263 TGCCTTCAGCCAGGGCTCCTCGCTCTTTAAGCACCAGCGCGTGCACACAGGCGAGAAGCC 1322
                                                                                           178 TGCAGCCGGCGAGAGCTCCAGCTCCGACCCGCGCGCCCCGCGTTCCCCAGGAGGTTCAT 237
                    238 CTGCTCCTTCCCTGACTGCAGCGCCAATTACAGCAAAGCCTGGGAAGCTTGACGCGCACCT 297
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CTTCGCCTGCCCACAGTGCGGCCGCCCTTTAGCCACAGCTCCAACCTCACCCAGCACCA 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGCACTACCGCACACACGGGCGAGAAGAAGTT 1058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCCACATTCTGACTCACACAGGAGAAAAGCCGTT 414
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                                                                                                                                                  Conservative
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48.9%;
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54.6%;
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                                                                                                                                                                   Score 58.8; DB 4;
Pred. No. 4.1e-06;
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                                                                                                                                                Mismatches 112;
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                                                                                                                                                                                     DB 4;
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                                                                                                                                                                                   Length 2992;
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: LOCATION: (0)...(0)
: OTHER INFORMATION: Zic 1 Protein gene; Genbank Acession D76435
US-09-234-332-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
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LENGTH: 3138
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                  Sequence 1, Application Patent No. 5981217
GENERAL INFORMATION:
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Best Local Similarity 55.2%;
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Michel F. Levesque, M.D.
APPLICANT: TOOMBS Neuman, Ph.D.
TITLE OF INVENTION: CONVERSION OF NON-NEURONAL CELLS INTO
TITLE OF INVENTION: NEURONS; TRANSDIFFERENTIATION OF EPIDERMAL CELLS
FILE REFERENCE: P07 41494
CURRENT APPLICATION NUMBER: US/09/234,332A
CURRENT FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 16
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman
STREET: P.O. Box 293
                                                                                                          APPLICANT: Subramaniam, M.
APPLICANT: Spelsberg, T. C.
TITLE OF INVENTION: DAR ENCONDING TGF-BETA INDUCIBLE
TITLE OF INVENTION: EARLY FACTOR-1 (TIEF-1), A GENE |
                                                                 NUMBER OF SEQUENCES:
                                                                                       TITLE OF INVENTION: BY OSTEOBLASTS
                                                                                                                                                                                                                                                                                                                                                               1822 GACCGCAAGAAGCA 1835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCTGTGGCAAGGTCTTCGCGCGCTCCGAGAATTTAAAGATCCACAAAAGGACGCACACA 1761
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                                                                                                                                                                                                                                                Application US/08570227A
                                                                                                                                                      Subramaniam, M.
Schwegman,
O. Box 2938
                   Lundberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       437
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                     Woessner &
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                     Kluth,
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COMPUTER READABLE FORM

55402

COUNTRY:

USA

Minneapolis MN

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APPLICANT: Subramaniam, M.

APPLICANT: Spelsberg, T.C.

APPLICANT: Roche, P.C.

TITLE OF INVENTION: TGF-Beta inducible early factor-1

TITLE OF INVENTION: (TIEF-1) and a method to detect brea

FILE REFERENCE: 150.1570S2

CURRENT APPLICATION NUMBER: US/09/077,991

CURRENT FILING DATE: 1998-07-07

EARLIER APPLICATION NUMBER: PCT/US96/19555

EARLIER FILING DATE: 1996-12-11

EARLIER APPLICATION NUMBER: US 08/570,227

EARLIER FILING DATE: 1995-12-11

NUMBER OF SEQ ID NOS: 13

COPTUDED: Paster For Windows Version 3.0
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US-09-077-991-1
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Best Local Similarity 54.6%;
Matches 106; Conservative
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                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09077991
Patent No. 6207375
SOFTWARE: FastSEQ for Windows Version 3.0
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SEQUENCE CHARACTERISTICS:
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FILLING DATE: 11-DEC-19
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1185 AGGAGTCACATCTGTAGCCACCCAGGATGTGGCAAGACATACTTTAAAAGTTCCCATCTG 1244
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REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 150.157US1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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Pred. No. 0.00013;
                                                                                                                                                                                               detect breast cancer
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-077-991-1
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Best Local Similarity 54.6%;
Matches 106; Conservative
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                                                                                                                                                  FILING DATE: 26-AUG-1991
ATTORNATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 3047
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                       INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, APPLICANT: FALKNER, F. G
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                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                  SEQUENCE CHARACTERISTICS:
TOPOLOGY: line
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Balance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 100.
CTTY: Alexandria
                                                                                                                    TELEX:
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                              LENGTH:
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                                                                                                                      899149
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1800 Diagonal Road,
                                                                7218 base pairs
                                                                                                                                       (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.25
                 linear
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                                                                                                                                                                                                                                                                               EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                 US/07/935,313
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Pred. No. 0.00013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suite 500
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; LOCATION: (79)...(3399)
US-09-657-042A-3
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US-09-657-042A-3
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US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/657,042A
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 3
LENGTH: 3600
                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09657042A Patent No. 6329203
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                                                                                                                                                                                                                          Matches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: C. Frank Ben
APPLICANT: Jacqueline Wyatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                     1057
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                                                                                      997
                                                                                                                                                  937 ATGCTGGTTGCACATGCGCAGACACACTGGCGAGAAGCCACACAAGTGCACGTTTGAA 996
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                                                                                                      GGGTGTGGCAAGGCCTTCATCAGGGACTACCATCTGAGCCGCCACATTCTGACTCACACA 400
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                     GGTGAGAAGCCATACATGTGTGAGCACGAGGGCTGCAGTAAAGCCTTCAGCAATGCCAGT 1116
                                                                                    GGGTGCCGGAAGTCATACTCACGCCTCGAAAACCTGAAGACGCACCTGCGGTCACACACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. Frank Bennett
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                                                                                                                                                                                                                      Score 52.6; DB 4; Length 3600; Pred. No. 0.0002; 0; Mismatches 139; Indels 3
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; LOCATION: (572)...(4348)
US-09-907-843-3
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US-08-946-241B-1
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US-09-907-843-3
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APPLICANT: C. Frank Bennett

APPLICANT: Susan M. Freier

TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-2 EXPRESSION
                                                                                                                                                                                                                                   Sequence 1, Application US/08946241B Patent No. 5928941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/907,843
CURRENT FILING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 3
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                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: McA'Nulty, Megan M.
APPLICATI: MCA'Nulty, Megan M.
APPLICATION: REPRESSOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: HOMO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 4960
TYPE: DNA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                               STREET: 225 I
                                                                  STATE:
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ses 136; Conserv
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                                                                                                                                                                    REPRESSOR KRUPPEL-LIKE FACTOR
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Pred. No. 0.00063;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: WCA'NULTY, Megan M.
TITLE OF INVENTION: REPRESSOR KRUPPEL-LIKE FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,241B
FILLING DATE: 07-CCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/030,035
FILING DATE: 05-NOV-1996
APPLICATION NUMBER: 60/027,521
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/946,241B FILING DATE: 07-0CT-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/030,035
                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1594 CACTTGTGATTACGCGGGCTGCGGCAAAACCTACACAAAGAGTTCCCCATCTCAAGGCACA 1653
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LENGTH: 1889 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                    PRIOR APPLICATION DATA:
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TELEFAX: vi.
200154
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LOCATION:
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                                                                                                                                                                                                                                          STREET: 225 |
CITY: Boston
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  APPLICATION NUMBER:
                                                                                                                                                                                                       COUNTRY:
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60/030,035
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                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: Mc4'Nulty, Megan M.
TITLE OF INVENTION: REPRESSOR
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                                                                                                        AFFLIANT DATE:
FILING DATE:
PRIOR APPLICATION NUMBER: 08,
APPLICATION NUMBER: 07-007-019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 05-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                  SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                              FILING DATE: 07-OCT-1997
APPLICATION NUMBER: 60/0
FILING DATE: 05-NOV-1996
                                                                                                                                                                                                                                                     MEDIUM TYPE:
COMPUTER: II
                                               APPLICATION NUMBER: 60/0 FILING DATE: 07-OCT-1996
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TELEFAX: 617-542-8906
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REGISTRATION NUMBER:
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                                                                60/027,521
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34,310
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05433/027001

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TELEFAX: 200154
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1889 base pairs
TYPE: nucleic acid
TYPE: nucleic single
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US-09-309-053-8
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Best Local Similarity
Matches 99; Conserv
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APPLICANT: Lee, Mu-En
APPLICANT: McA'NuLty, Megan M.
TITLE OF INVENTION: REPRESSOR KRUPPEL-LIKE FACTOR
                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/946,241
FILING DATE: 07-OCT-1997
APPLICATION NUMBER: 60/030,035
FILING DATE: 05-NOV-1996
APPLICATION NUMBER: 60/027,521
APPLICATION OMBER: 60/027,521
FILING DATE: 07-CCT-1996
ATTORNEY/AGENT INFORMATION:
INFORMATION FOR SEQ ID NO:
                                                           NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: EastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                 TELEFAX: 02.54
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CITY: Boston
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Search completed: February 10, 2003, 12:48:08 Job time: 109.257 secs
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Best Local Similarity 55.0%;
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LENGTH: 1889 base pairs
TYPE: nucleic acid
STRANNEDNESS: single
TOPOLOGY: linear
                                                                                  1714 ATTCGCCCGCTCAGATGAACTGACCAGGCACTACCGTAAACACACGGGGCCACCGCCCGTT 1773
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LOCATION:
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Pred. No. 0.00059; 
0; Mismatches 81; Indels
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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  3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/US00_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US00_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
GenCore version
(c) 1993 - 2003
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14 US-09-920-300A-610
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16 US-09-95-973-2
10 US-09-95-973-2
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10 US-09-95-973-348-4
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Sequence 2, Appli
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Sequence 1175, Ap
Sequence 1177, Ap
Sequence 1747, Ap
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Sequence 689, App
Sequence 689, App
Sequence 4064, App
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Sequence 119, App		Sequence 1716, Ap	Sequence 137, App	Sequence 73, Appl	Sequence 120, App	Sequence 1613, Ap	Sequence 950, App	Sequence 17, Appl	Sequence 4, Appli	Sequence 16, Appl	Sequence 642, App	Sequence 4925, Ap	Sequence 417, App	Sequence 211, App	Sequence 28, Appl	Sequence 17, Appl	Sequence 29, Appl	Sequence 1647, Ap	Sequence 4943, Ap	Sequence 76, Appl	Sequence 10, Appl	2	Sequence 14, Appl	Sequence 14, Appl	Sequence 14, Appl

## ALIGNMENTS

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; ORGANISM: Homo
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LENGTH: 439
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Best Local Similarity 99.8%;
Matches 419; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 326, Application US/09920300A
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APPLICANT: Meagher, Maddeleine
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.547
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                ACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGATCCTGACAAGAAG 1033
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Pred. No. 1.4e-103;
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APPLICANT: King, Gordon E.
APPLICANT: Weagher, Madeleine Joy
APPLICANT: Weagher, Madeleine Joy
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547C1
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
NUMBER OF SEQ ID NOS: 1896
SOFTMARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 326
LENGTH: 439
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; Patent No. US20020136728A1
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; ORGANISM: Homo sapiens
US-10-033-528-326
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Pred. No. 1.4e-103;
O; Mismatches 1;
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Best Local Similarity 99.5%;
Matches 418; Conservation
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NUMBER OF SEQ ID NOS: 1789

SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 689
LENGTH: 439
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                    SEQ ID NO 689
LENGTH: 439
                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  Sequence 689, Application US/10033528 Patent No. US20020131971A1
   Query Match
                                                                                                                                                      TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.547C1

CURRENT APPLICATION NUMBER: US/10/033,528

CURRENT FILING DATE: 2001-12-26
                                                                                                                                                                                                                                              APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine
APPLICANT: We Jiangchun
APPLICANT: Secrist, Heather
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APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547
CURRENT APPLICATION NUMBER: US/09/920,300A
                                                                                                                          SOFTWARE: FastSEQ for Windows Version
                                                                                                                                         NUMBER OF SEQ ID NOS:
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                                                    TYPE: DNA ORGANISM: Homo sapiens
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Pred. No. 3.7e-103;
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   Score 416.8;
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CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR PRIOR DATE: 2000-03-17
PRIOR PRIOR DATE: 2000-03-17
PRIOR FILING DATE: 2000-04-27
PRIOR TILING DATE: 2000-04-27
PRIOR PPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-8
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/206,201
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSEQ for Windows Versio
SEQ ID NO 4064
LENGTH: 234
                                                                                                                    PRIOR APPLICATION NUMBER: 60/218,950 PRIOR FILING DATE: 2000-07-14 PRIOR APPLICATION NUMBER: 60/222,903 PRIOR FILING DATE: 2000-08-03 PRIOR APPLICATION NUMBER: 60/223,416 PRIOR FILING DATE: 2000-08-04 PRIOR FILING DATE: 2000-08-04
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RESULT 7
US-10-033-528-610
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LENGTH: 234
TYPE: DNA
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Best Local Similarity
Matches 234; Conservat
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CURRENT FILLING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1799
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 7.1e-54;
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APPLICANT: Xu, Jiangchun

APPLICANT: Secrist, Heather

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210121.547C1

CURRENT APPLICATION NUMBER: US/10/033,528

CURRENT FILING DATE: 2001-12-26

NUMBER OF SEQ ID NOS: 1896

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 610

LENGTH: 234
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Burmer, Glenna C.
APPLICANT: Burmer, Goeph P.
TITLE OF INVENTION: Nucleic Acid Sequences A.
TITLE OF INVENTION: Nucleic Acid Sequences A.
TITLE OF INVENTION: Number: US/09/292,758
FILE REFERENCE: 017473-001110US
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: US/09/292,758
CURRENT FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 147
SOFTWARE: FASTESEQ for Windows Version 3.0
SEQ ID NO 68
LENGTH: 362
TYPE: DNA
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US-09-292-758-68
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Best Local Similarity
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Best Local Similarity
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                  1003 GCATGCTGTTGTACATGATCCTGACAAGAAGAAAATGAAGCTC-AAAGTCAAAAAAATCTC 106:
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                                                                      TGTGTGTGAACATGCTGGCTGTGGCAAAAACATTTGCAAATGAAACAAAGTCTCACTTAG 303
                                                                                        TGTGTGTGAACATGCTGGCTGTGGCAAAA--CATTTGCAATGAAACAAAGTCTCAC-TAG 1002
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Pred. No. 1.3e-51;
0; Mismatches 5
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US-09-995-973-2
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LENGTH: 947
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Best Local Similarity 57.6%;
Matches 273; Conservative
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APPLICANT: UTLMAN, Christopher G.
APPLICANT: UTLMAN, Christopher G.
TITLE OF INVENTION: GENE SWITCHES
FILE REFERENCE: 8325-2003 / G7-US1
CURRENT APPLICATION NUMBER: US/99/995,973
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NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver. 2.0
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CCGCTTTTCTCGCTCGGATGAGCTTACCCGCCATATCCGCATCCACACACGCCA 499
                      ACACTTTGCATCACCCAGCAAGCTGAAAACGACATGCCAAGGCCCACGAGGGCTA 681
                                                                   TCATCAGTTCAGTCACACAGCAGCTGCCGTATGCCTTGCCCTGTCGAGTCCTGCGATCG
                                                                                                     ATATATATGCAGTTTTGAAGACTGTAAGAAGACCTTTAAGAAACATCAGCAGCTGAAAAT 567
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Pred. No. 1.9e-31;
0; Mismatches 201;
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RESULT 10 US-09-732-348-5

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; Sequence 1, Application US/09995973; Publication No. US20030024006A1
; GENERAL INFORMATION:
; APPLICANT: CHOO, Yen
; APPLICANT: ULLMAN, Christopher G.
; TITLE OF INVENTION: GENE SWITCHES;
; FILE REFERENCE: 8325-2003 / G7-US1
; CURRENT APPLICATION NUMBER: US/09/995,973
; CURRENT FILING DATE: 2002-03-19
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US-09-995-973-1
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CURRENT FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 21
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TITLE OF INVENTION: Regulated Gene Expression
FILE REFERENCE: 674538-2001
FILE REFERENCE: 674538-2001
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LOCATION: (723)..(908)
OTHER INFORMATION: transactivation domain of VP64, other features ex
OTHER INFORMATION: listed below) same as SEQ ID NO:
NAME/KEY: misc_feature
LOCATION: (909)..(938)
OTHER INFORMATION: c-myc tag, other features except transactivation
OTHER INFORMATION: ted above) same as SEQ ID NO:
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TYPE: DNA
ORGANISM: Artificial Sequence
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Local Similarity 57.6%;
es 273; Conservation
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Pred. No. 1.9e-31;
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US-09-732-348-4
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SEQ ID NO 1
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LENGTH: 995
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                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                            TYPE: DNA
                  NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                 446
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OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: TFIIIA/Zif-VP16
US-09-995-973-1
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Local Similarity 57.6%;
les 273; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGCAAAGCCTGGAAGCTTGACGCGCACCTGTGCAAGCACACGGGGGGAGAGACCATTTGT 327
CCGCTTTTCTCGCTCGGATGAGCTTACCCGCCATATCCGCATCCACACACGGCCA 499
                              ACACTTTGCATCACCCAGCAAGCTGAAAACGACATGCCAAGGCCCCACGAGGGCTA 681
                                                                                                                                                                                                                                                                                                                TACTACAAAGGCAAACATGAAGAAGCACTTTAACAGATTCCATAACATCAAGATCTGCGT
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                                                                                                     TCATCAGTTCAGTCACACACAGCAGCTGCCGTATGCCTTGCCCTGTCGAGTCCTGCGATCG
                                                                                                                                                     ATATATATGCAGTTTTGAAGACTGTAAGAAGACCTTTAAGAAACATCAGCAGCTGAAAAT
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Sequence 4, Application US/09732348
Patent No. US20020046419A1
                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 21 SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/732,348 CURRENT FILING DATE: 2000-12-07
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Yen Choo, et al.
TITLE OF INVENTION: Regulated Gene Expression
FILE REFERENCE: 674538-2001
NAME/KEY: misc_feature
LOCATION: (15)..(17)
OTHER INFORMATION: translational
NAME/KEY: misc_feature
LOCATION: (16)..(416)
OTHER INFORMATION: Fingers 1 to 4
                                                                                    initiating
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: NAME/KEY: misc_feature
: LOCATION: (417)...(689)
: OTHER INFORMATION: three fingers of
: NAME/KEY: misc_feature
: LOCATION: (701)...(722)
: OTHER INFORMATION: unclear Localize
: NAME/KEY: misc_feature
: LOCATION: (957)...(986)
: OTHER INFORMATION: c-myc tag
US-09-732-348-4
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                               SOFTWARE: Patentin Ver.
SEQ ID NO 5443
LENGTH: 449
                                                                                                                                                                                                                                                                                                                Sequence 5443, Application Patent No. US20020110850A1 GENERAL INFORMATION:
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Best Local Similarity 57.6%;
Matches 273; Conservative
                                                                                 CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR PILING DATE: 1994-11-21
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
                                                                                                                                                                                                  APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences,
FILE REFERENCE: PO-16.2C1
                                                                                                                                                                                                                                                APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William
APPLICANT: L1, Haddong
APPLICANT: Rosen, Craig A.
ORGANISM: Homo sapiens
                     TYPE: DNA
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Pred. No. 1.9e-31;
0; Mismatches 201;
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
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                                                                                                                                                                                                                                                                                                                              TGNAACCTCTATTCCAAGTGTACCCAGGGAAGGATGTGGGAAACACTTTGGCATTCACCC
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                                                                 TNCNTTGTGGGCAAAAACTGGGACGGGACTTCTGNAACTGTGAGNGAAACCCTTAAGGGG
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                                                                                                                                                                                                                                                                                  -GAAGACCTTTAAGAAA-----CATCAGCAGCTGAAAATCCATCAGTGCCAGCATACCAA 588
                                                                                               TCCTTTGTGGCAAAAACATGGACGGAACTTCTGAAACATGTGAGAGAAACCCATAAAGAG
                                                                                                                                                                                                                                                                                                                                                                                               TTGNGCAGCCAATGGCTTGANATCAAAAATTCAACACAAAATCAAACTTGAAGAAACATT 122
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US-09-920-300A-1747/c

; Sequence 1747, Application US/09920300A

; Patent No. US20020136728A1
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; NAME/KEY: misc_feature
; LOCATION: (1)...(1111)
; OTHER INFORMATION: n = A,T,C or
US-09-833-381-1175
; NAME/KEY: misc_feature
; LOCATION: 223, 323
: OTHER INFORMATION: n - A,T,C or
US-09-920-300A-1747
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Sequence 1175, Application US/09833381
Patent No. US20020132090A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SEO ID NO 1175
LENGTH: 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1747
LENGTH: 368
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Best Local Similarity 61.1%;
Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeline Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
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                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Prcd. No. 1.3e-13;
0; Mismatches 89; Indels 0;
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                                                                        296 CATGTGAGAGAAACCCATAAAG 275
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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### ALIGNMENTS

REFERENCE AUTHORS		ORGANISM		SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	HUMITIA	RESULT 1
l (bases 1 to 1381) Arakawa,H., Nagase,H., Hayashi,N., Ogawa,M., Nagata,M.,	<pre>Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</pre>	Homo sapiens	and Y.Nakamura clone:39H11.	Homo sapiens cDNA to mRNA, clone_lib:librarry of T.Fujiwara, S.Shin	GTF3A; Xenopus transcription factor IIIA homologue.	D32257.1 GI:1000446	D32257	complete cds.	Human GTF3A mRNA for Xenopus transcription factor IIIA homologue,	HUMIIIA 1381 bp mRNA linear PRI 07-FEB-1999		

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TGCAGCCACTGGCTGTGATCAAAAATTCAACACAAAATCAAACTTGAAGAAACATTTTGA
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                                                                CTCCTTCCCTGACTGCAGCGCCAATTACAGCAAAGCCTGGAAGCTTGACGCGCACCTGTG
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Submitted (22-UUL-1994) Yusuke Nakamura, Cancer Institute,
Submitted (21-UUL-1994) Yusuke Nakamura, Cancer Institute,
Department of Biochemistry; 1-37-1 Kami-Ikebukuro, Toshima
Tokyo 170, Japan (E-mail:nakamuraéganvxl.jfcr.or.jp,
Tel:03-3918-0111(ex.4501), Fax:03-3918-0342)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fujiwara, T., Takahashi, E., Shin, S. and Nakamura, Y. Molecular cloning, characterization, and chromosomal mapping novel human gene (GTF3A) that is highly homologous to Xenopus transcription factor IIIA Cytogenet. Cell Genet. 70 (3-4), 235-238 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakamura, Y
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//db_xref="MRSGCADAGRCLVTARAPGSVPASREGSAGSRGPGARFPARVSA RGSAPGPGLGAGALDPPAVLASVSSLTIADAFIAACESSAPTPPRDALPRRFICSF PDCSANVSKAMKLDAHLCKHTGEREFVCDYECGKCKTERKHQQLKIHGCQNTNEP PDCSANVSKAMKLDAHLCKHTGEREFVCDYCOKGCSFVAKTWTELLKHVRETHKEEIL CEVCRKTERKEDLLKHVRETHKEEIL CEVCRKTERKEDLLKHNKTHAPERDVCRCPRGCGRTYTTVFNLQSHILSFHEESER PCCHAGCGKTFAKKOSLTRHAVVHDDPKKKMLKVKKSREKREFGLSSQMIYPPKRK OGQGLSLCQNGESPNCVEDKMLSTVAVLTLG"

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/db_xref="taxon:9606"
/clone="39H11"
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Hc
2 1 (bases 1 to 1399)
5 FUjiwara, T. Takeda, S., Shimada, Y., Ozaki, K. and Shin, 7
HUMAN TRANSCRIPTIONAL FACTOR IIIA GENE
L Patent: JP 196070870-A 1 19-MAR-1996;
OTSUKA PHARMACEUT CO LTD
OS Homo Sapiens (human)
PN JP 1996070870-A/1
PD 19-MAR-1996
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Becker,K.G.
Cloning and expression a
Xenopus TFIIIA
Gene 159 (2), 215-218 (1
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U20272.1
                                                                                                           Submitted (25-JAN-1995) Kevin G. Becker, Diseases and Stroke/NIH, Neuroimmunology Pike, Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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       /sex "female"
/tissue_type="brain; hippocampus"
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<1. 1092
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/db xref = "taxon:9606"

/clone= "C2H2-34.10"

/sex = "form = 1 - "
/note="similar to Xenopus
                                                                                                  Location/Qualifiers
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/protein_id="AAA75623.1"
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CEHAAGGKTFAMKOSLTHAVYHDPDKKKKKLKVKKSREKRSLASHLSGYIPFKRKOG
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                                                                                                                                                                 Submitted (29-AUG-1994) Kevin G. Becker, National Institute
                                                                                                                                                                                Direct Submission
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Number 936205"
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/db_xref="taxon:9606"
/clone="C2H2-34"
/sex="2 yr old female"
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                                                                                         TCCTTCCCTGACTGCAGCGCCAATTACAGCAAAGCCTGGAAGCTTGACGCGCACCTGTGC
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/note="encodes :
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/gene="HTFIIIA"
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/note="encodes zinc-finger"
394. .462
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/note="encodes zinc-finger"
208. .276
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263 c 244 g 252 t
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/note="encodes zinc-finger"
490. .558
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CSANYSKAWKIDAHLCKHTGERPFVCDYEGCGKAFIKDHLSRHILTHTGEKPFVCDX
NGCDDKFWTKSLUKKHTGERKHENQOKOYICSFEDCKKTFKKHQULKIHQCOHTNEPLF
KLCCQKGCSFVAKTWTELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPERDV
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/protein_id="AAA21873.1"
/db_xref="GI:551535"
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/note="TFIIIA; similar to Xenopus transcription
IIIA, Swiss-Prot Accession Number P03001"
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AK057993. GI:16553988
AK057993.1 GI:16553988
Oligo Capping; fis (full insert sequence).
Homo sapiens stomach mucosa cDNA to mRNA, clone\_lib:STM clone:STM05057. AK057993 1920 bp Homo sapiens cDNA FLJ25264 fis, TRANSCRIPTION FACTOR IIIA. clone mRNA linear PRI 31-OCT-2001 one STM05057, highly similar to

Homo sapiens

Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M., Yamashita,H., Chiba,Y., Suzuki,Y., Hata,H., Nakagawa,K., Mizuno, Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato, Morinaga,M., Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., and Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiguchi,S., Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M., Yamashita,H., Chiba,Y., Suzuki v Sugano, S. NEDO human cDNA sequencing project Chordata; Primates; Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. ŝ Sato, H.,

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                                                                             TCGCTGTCCAAGAGAAGGCTGTGGAAGAACCTATACTACTGTGTTTAATCTCCCAAAGCCA 912
                                                                                                                                                       TAAACGCAAAGATTACCTTAAGCAACACATGAAAACTCATGCCCCAGAAAGGGATGTATG
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                  GAAACATGTGAGAGAAACCCATAGAGGAGGAAATACTATGTGAAGTATGCCGGAAAACATT
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Direct Submission
Submitted (24-0CT-2001) Sumio Sugano, Institute of Medical Science, Submitted (24-0CT-2001) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of Resonomy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Science, University of Tokyo, Laboratory of Genome Structure, Human
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Sugano, S. and Suzuki, Y
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/clone_lib="STM"
/note="cloning vector: pME185
462 c 438 g 500 t
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/clone="STM05057"
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Hanas, J.S., Hocker, J.R., Lerner, M.R., Brackett
LightCoot, S.A., Hanas, R.J., Maduhadson, K. and
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (14-JUN-2001) Blochemistry/Molecular Biology, University of Oklahoma Health Science Center, 800 Research Parkway, Suite 448,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanas,J.S., Hocker,J.R., Cheng,Y.G., Lerner,M.R., Brackett,D.: Lightfoot,S.A., Hanas,R.J., Madhusudhan,K.T. and Moreland,R.J. CDNA Cloning, DNA binding, and evolution of mammalian transcri
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                                                                  RDVYRCPROGCGRTYTTVFNLQSHILSFHEEKRPFVCEHAGCGKTFAMKQSLMRHSVV
HDPDKKRMKLKVRAPRERRSLASRLSGYFPPKRKQEPDYSLPNASAESSSSPEAQLPP
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GAGGGCTGTGGCAAAGCCTTCATCAGGGACTACCATCTGAGTCGACACATCCTGATTCAC
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Submitted (14-JUN-2001)
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Lightfoot, S.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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nas_J.S., Hocker,J.R., Lerner,M.R., Brackett,D.
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/protein_id="AAL69885.1"
/protein_id="AAL69885.1"
/db_xref="GI:18448380"
/translation="AAR6ALPSRFTCSFPDCSASYNKAWKLDAHLCKHTGERSFVCD
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/translation="AARAC
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/db_xref="taxon:10116"
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IMAGE:5374268,
    Direct
                   Strausberg, R.
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    Submission
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                                         Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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TTTGTTGTGCAGCCACTGGCTGTGATCAAAAATTCAACACAAAATCAAACTTGAAGAAA 472
                                                                                     CACATTGAACGCAAACATGGAAACCCCACAAAAACAGTATGTGTGCAGTTATGAGGGTTGC
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This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: nisc_mgo@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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/protein_id="AAH32292.1"
/db_xref="GI:21595508"
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old mouse. Taken by biopsy."
/clone_lib="NCI_GGAP_Mam2"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mGKTWTELLKHMREAHKEDITCNVCORMFKRRDYLKOHMKTHAP
ERDVYRCPROGCGRTYTTVFNLOSHILSFHEEKRPFVCEHAGCGKTFAMKOSLMRHSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                                              Waterston, R.
Direct Submission
Submitted (23-MAY-1998)
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AC004739
AC004739.1 GI:31
                             Submitted (03-FEB-2000) Department of Genetics, University, 4444 Forest Park Avenue, St. Louis,
                                                                                                  University, 4444 Forest 3 (bases 1 to 97979)
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                                                                                                                Department of Genetics,
Park Avenue, St. Louis,
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Center code: wVGSC
web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
Contact: Summary Statistics
Center project name: H_DJ053IG15
Center project name: H_DJ053IG15
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

#### MAPPING INFORMATION: The sequence of this

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Bric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center: For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CH7, send mailto:egreen@nhgri.nih.gov/DIR/GTB/CH7, send

# SOURCE INFORMATION:

This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at Roswell Park Cancer Institute, using the method described by Joannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor. For further details, see http://bacpac.med.buffalo.edu/
The clone is available from Genome Systems, Inc.
(http://www.genomesystems.com).
VECTOR: PCYPAC2
NEIGHBORING SEQUENCE INFORMATION:
The actual start of this clone is at base position 1 of RP4-531G15 actual end is at base position 97979 of RP4-531G15.

FEATURES source repeat\_region This clone contains STS swSS2758
Location/Qualifiers /rpt\_fami 8397. .87 /rpt\_family="L1" 9751. .12094 /rpt\_family="MIR" 3238. .3572 /rpt\_family="L2" 660. .831 /rpt\_family="MIR" 7085. .8157 /rpt\_family="Alu" 12373. .12436 /rpt\_family="Alu" 3868. .4067 /db\_xref="taxon:9606" /chromosome="7" /rpt\_family="(CA)n" 12095 rpt\_family="Alu /clone\_lib="RPCI-4" /clone="RP4-531G15" /map="7p21" ∕organism≖"Homo sapiens family-"L1" .12436 .12372 Lly="L1" y="Alu (NID:g1113567)

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43023. .43418
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42711. .43026
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38302. .38768
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37910. .38123
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33843 .33929
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32178. .32319
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21491. .21543
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18044. .18633
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16679, .16732
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44534. .45153
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Submitted (05-MAY-1999) Genome Sequencing Center, Washing
University School of Medicine, 4444 Forest Park Parkway,
MO 63108, USA
On May 5, 1999 this sequence version replaced g1:3907455.
Location/Qualifiers
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Homo sapiens clone NH0547G15,
AC006045
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Submitted (22-NOV-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
3 (bases 1 to 193126)
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         -AATTCAACACAAAATCAAACTTGAAGAAACATTTTGAACGCAAACATGAAAATC
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Mammalia; Eutheria; Primates;
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Sulston,J.E. and Waterston,R.
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FEATURES SOURCE		TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL COMMENT
The clone sequenced to the left is CTD-2105K18, 2000 bp overlap; the clone sequenced to the right is RP11-533K11, 2000 bp overlap. Actual start of this clone is at base position 141753 of CTD-2105K18; actual end is at base position 16829 of RP11-533K11.  Polymorphisms have been identified between AC016444 and AC074390. Data from AC016444 was used to finish this clone, AC074390. 1. 11172 2 /organism="Homo Sapiens" /db_xref="taxon:9606" /chromosome="7" /clone="RP11-515K14"	NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.  MAPPING INFORMATION:  The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center: For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov/DIR/	Direct Submission Submitted (30-JUL-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 4 (bases 1 to 111722) Waterston,R.H. Direct Submission Submitted (19-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 5 (bases 1 to 111722) Waterston,R. Direct Submission Submitted (21-FEB-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA on Jan 19, 2002 this sequence version replaced gi:17976493.  Center: Washington University Genome Sequencing Center Center code: WUCSC Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu Center project name: H_NHO515K14
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JOURNAL REFERENCE
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                                                                                                                                                                                Submitted (26-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 9, 2000 this sequence version replaced gi:6778507. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 11, clone RP11-384114
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                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                 Contact: sequence_submissions@genome
----- Project Information
Center project name: L5006
                                                                                                                               Center: Whitehead Institute/ MIT Center code: WIBR
Center clone name: 384_I_14
                                                                                                  Web site: http://www-seq.wi.mit.edu
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127925 128024: gap of 100 bp
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Insert size: 205122; sum-of-contigs
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88 16287: gap of 100 bp
18 18628: contig of 2341 bp
29 18728: gap of 100 bp
29 2545: contig of 3817 bp
46 22645: gap of 100 bp
46 22645: gap of 4688 bp
                                     /note="assembly_fragment"
27434. .32718
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14859. .16187
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162338: contig of 34314 bp in length
52438: gap of 100 bp
206622: contig of 44184 bp in length
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/note="assembly_fragment"
80935. .102411
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58236. .69592
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vector_side:right"
34710 c 35722 g
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Query Match Best Local Similarity Conservative 37.3%; 0 Score 452.6; DB 2; Pred. No. 6.2e-91; Mismatches 139; Indels Length 206622 29; Gaps 12;

36308 CCCCTTCACACACTTCTTAGGAGGGTCATCTGCTACTTCCC-CAGTGTGGCACCACTTAC 269 AGCAAAGCCTGGAAGCTTGACGCGCACCTGTGCAAGCACGGGGGGAGAGACCATTTGTT 328 209 CCGCCCCCCCCCCTTCCCAGGAGGTTCATCTGCTCCTTCCCTGACTGCAGCGCCAATTAC TATGACTGTGAAGGGTGTGGCAAGACCCACCTCAAGAGACTAACATCTGAGTTGTCATGT TGTGACTATGAAGGGTGTGGCAAGGCCTTCATC-AGGGACTACCATCTGAGCCGCCACAT 387 AAAAAGGCCTGGAAGCTTAATGTGCACCTGT--AATCACATGGGGAAGAAACCATTTGTT 36484 36424 36366

TCTGACTCACACAGAGAAAAGCCGTTTGTTTGTGCAGCCACTGGCTGTGATC-AAAAAT 446 TCAACACAAAATCAAACTTGAAGAAAACATTTTGAACGCAAACATGAAAAATCAAAAAAAC 506 36603

A----ATATATATGCAGTTTTGAAGACTGTAAGAAGACCTTTAAGAAACATCAGCAGCT 561

AAAAATATACATATGCAATTTTGGAGGTTGGAAGAAGACCTTTACG-AACATCAGCAGCT 36662

FEATURES

TGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACATGCCAAGGCCCACGAGGGCTA 36722

TGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGGACGGAACTTCTGAAACATGT TGGGAAGCATTTTTCCCCCATCCATCCAGC-----AAGCGGCCAAGGCCCCATGCGGGCTC 741 36775

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--ATTATCTTAAGCAACATATGAACACTCATGCCCCCAGAAAGGGATAT-TTTTGACATAC GAGAGAAACTTATAAAAAGGAAACAACATATGAAGCAGGCCAGAAAACATTTAAAC----198 36891

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SOURCE
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AL353741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36949 AAGAGAAGTCTCTGGAAGAACCTACACAACTGTGTTTACTCTACAAATCCATATCCTTTC
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misc_feature
                                                                   misc_feature
                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                            rogether with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9 mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGATCCTGACAAGAAGAAGAAAATGAA 1041
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AL353741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (28-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humguery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/HGP/Chr9
RP11-575C20 is from the library RPCI-11.2 constructed of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Jan 28, 2001 this sequence version replaced gi:12580980. During sequence assembly data is compared from overlapping clones where differences are found these are annotated as variations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 199517)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                         left
                                                                                                                                                                                                                                                                                                                                     VECTOR: pBACe3.
                                                                                                                                                                                                                                                                                                                                                         http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laird, G
                                                                                                                                                                                                                                                            sequence is the entire insert of clone RP11-575C20 The true end of clone RP11-279E1 is at 116738 in this sequence. The right end of clone RP11-21817 is at 84470 in this sequence
                       /note*"Single clone region.
restriction digest data."
                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                      Location/Qualifiers
1. .199517
                                                                        159090
                                                                                       /clone_lib="RPCI-11.2"
                                                                                                                    /clone="RP11-575C20"
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                                                                                                                                           'Chromosome="9"
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#### ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL COMMENT KEYWORDS SOURCE ORGANISM RESULT 1 BM553401 LOCUS FEATURES DEFINITION VERSION ACCESSION source cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can i
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1968 row: o column: 07
High quality sequence stop: 673.
Location/Qualifiers Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP l (bases 1 to 1078)
NIH-MGC http://mgc.nci.nih.gov/.
NATI-MGC http://mgc.nci.nih.gov/.
NATI-MGC http://mgc.nci.nih.gov/.
NATI-MGC http://mgc.nci.nih.gov/.
NATI-MGC http://mgc.nci.nih.gov/.
NATI-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D. EST BM553401 1078 bp mRNA linear EST 20-FEB-2002 AGENCOURT\_6572564 NIH\_MGC\_41 Homo sapiens cDNA clone IMAGE:5467230 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens BM553401.1 GI:18792097 5', mRNA sequence. BM553401 human be

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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
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            ATGAACCTCTATTCAAGTGTACCCAGGAAGGATGTGGGAAACACTTTTGCATCACCCAGCA 647
                                                                                                                     ACTGTAAGAAGACCTTTAAGAAACATCAGCAGCTGAAAATCCATCAGTGCCAGCATACCA
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                                                                                                       ACTGTAAGAAGACCTTTAAGAAACATCAGCAGCTGAAAATCCATCAGTGCCAGCATACCA
Genoscope - Centre National de 9
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.coms.fr,
Location/Qualifiers
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Contact: Genoscope
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/clone="CSDDI057YN01"
/clone_115-"LYI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMYSPORT 6;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone="CSDDK0027J]8"
/clone="CSDDK0027J]8"
/clone="Lib="IT_NETD06.FUL2"
/tissue_type="placenta"
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AGENCOURT_6588903 NIH_MGC_98
5', mRNA sequence.
BM562682
                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae: 1 (bases 1 to 1059)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collegensialist
                     Unpublished (1999)
Contact: Robert Strausberg,
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Plate: LLCM1998 row: a column: 24
High quality sequence stop: 717.
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Wector: po?B7; Site_1: XhOI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhOI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
Callifornia, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
05 a 274 c 270 g 209 t 1 others
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AL574318 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODIO57YN01 3
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/note="Vector: pCMVSPORT 6; Site_1: Not1; 1st strand cDNA
/note="Vector: pCMVSPORT 6; Site_1: Not1; 1st strand cDNA
was primed with a Not1-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not 1 and
cloned into the Not 1 and Eco RV sites of the pcMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://primal.com/primal/pri
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Tissue Procurement: CGAP (Stenford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2478 row: j column: 20
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Contact: Robert St
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/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5 adaptor:
GCACGAG(G). Size-selected > 500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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prime, mRNA sequence.
AL527493
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Full-length cDNA libraries Unpublished (2001) Contact: Genoscope
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                                                                                 /note-"Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:
                                                   http://fulllength.invitrogen.com"
240 c 227 g 206 t
                                                                                                                                                                                                                                               /sex="male"
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Genoscope - Centre National de Sequencage
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111: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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//closue_type="placenta"
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                                                                                                                                     Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                               Helix Research Institute
1532-3 Yana, Kisarazu, Chiba
Tel: 81-438-52-3975
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/tlssue_type="whole embryo, mainly head"
/dev_stage="embryo, 10 weeks"
/note="Vector: pME18SFL3"
                                               /clone_lib="HEMBAl"
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information cai
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2484 row: j column: 14
High quality sequence stop: 642.
Location/Qualifiers
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BQ644275.1
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Tissue Procurement: CGAP (Stanford)
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NIH-MGC http://mgc.nci.nih.gov,
National Institutes of Health,
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/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
**Incolor**
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/clone="IMAGE:6285421"
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                                                                                                                                                                                                                                                                                                    Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization (npublished (2001) Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Location/Qualifiers
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                                          /clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Yector: pcMvSPORT 6; Site_1: NotI; 1st strand cDNA
/note="Yector: pcMvSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filang@lifetech.com URL:
http://eilboarth.com/URL:
                 http://fulllength.invitrogen.com"
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B0278693.1 GI:20488901
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Pred. No. 9.5e-174;
4; Mismatches 7;
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              GGCTGTGATCAAAAATTCAACACAAAATCAAACTTGAAGAAACATTTTGAACGCAAACAT
                                                                       AGCTCAGCTCCGACCCCGCCGCGCCCCCGCGCTTCCCAGGAGGTTCATCTGCTCCTTCCCT
                                           GGGGAGAGACCATTTGTTGTGACTATGAAGGGTGTGGCAAGGCCTTCATCAGGGACTAC
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Contact: Robert Strausberg, Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1089)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2044 row: f column: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: breast; vector: poTB7; Site_1: EcoRI;
Site_2: MhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/KhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CNAA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NHHMGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:5805333"
/clone_lib="NIH_MGC_107"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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94.6%;
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Pred. No. 1.8e-173;
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http://image.llnl.gov
Plate: LLCM1810 row: d column:
High quality sequence stop: 880.
                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                National Institutes of Health,
Unpublished (1999)
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/organism="Homo sapiens"
/db_xref="taxon:9666"
/clone="IMAGE:4906710"
/clone_lib="NIH_MGC_42"
/tissue_type="epithelioid c
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Pred. No. 4e-173;
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                                                              GAAAGCCCGCCTTTTGTGTGT
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TGCAGCCACTGGCTGTGATCAAAAATTCAACACAAAATCAAACTTGAAGAAACATTTTGA
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2449 row: f column: 19

High quality sequence stop: 608.

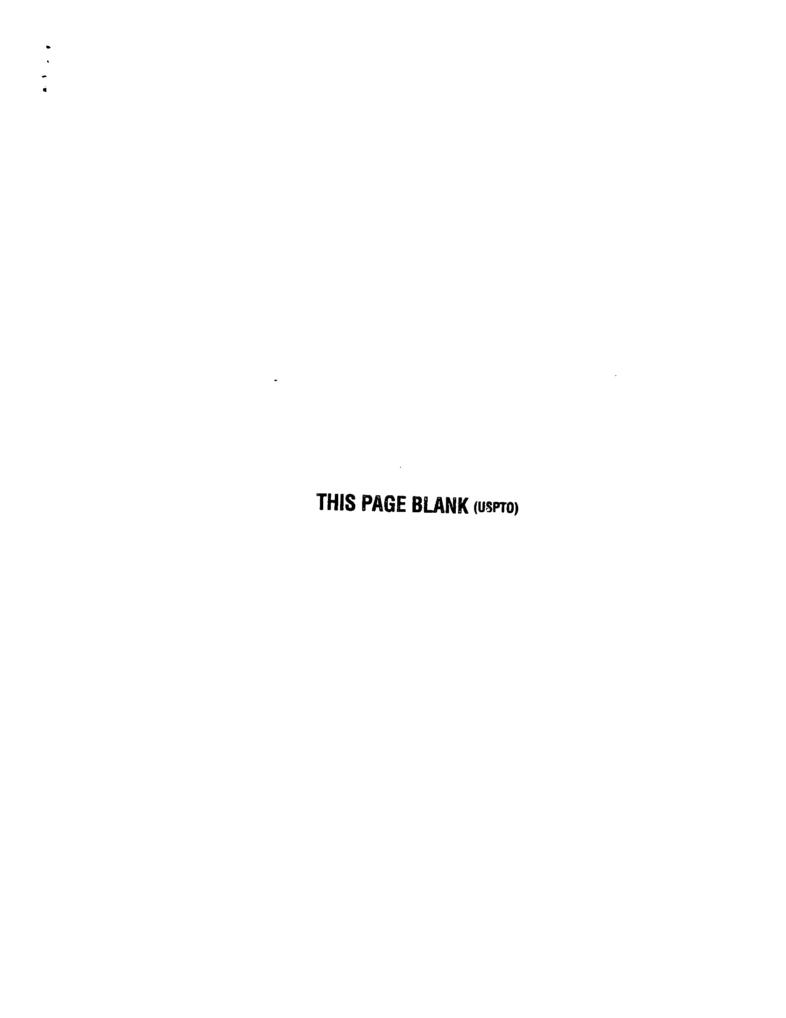
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BQ648620 908 bp mRNA linear EST 15-JUL-2002
AGENCOURT 8415143 NIH_MGC_100 Homo sapiens cDNA clone IMAGE: 6271890
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National institutes of Health, !
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/clone_llb="NMGE:6211890"
/clone_llb="NMGE:6211890"
/clone_llb="NH_MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DHIOB (phage-resistant)"
/lab_host="DHIOB (phage-resistant)"
/lab_host="DHIOB (phage-resistant)"
/lab_host="nHIOB (phage-resistant)"
/lab_host=
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Search completed: February 10, 2003, 17:44:18 Job time: 1907.59 secs

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4: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

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GENERAL INFORMATION:

APPLICANY: Compugen LTD

TITLE OF INVENTION. Variants of alternative spi

FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: PATENTIN VERSION 3.2

SEQ ID NO 93223

LENGTH: 430

TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676-93223
                                                                                                          Sequence 93234, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spiritize of INVENTION: Variants of alternative spiritize of Application US/09/724,676
CURRENT APPLICATION UNMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
UNMBER OF SEQ ID NOS: 97222
SOFTMARE: Patentin version 3.2
SEQ ID NO 93234
LENGTH: 430
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; ORGANISM: Homo sapiens
US-09-724-676-93245
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOPTWARE: PatentIn version 3.2
SEQ ID NO 93245
LENGTH: 430
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
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                   HDPDKKKMKLKVKKSREKRSLASHLSGYIPPKRKQGQGLSLCQNGESPNCVEDKMLSTVA
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Pred. No. 4e-176;
1; Mismatches
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Sequence 93256, Application US/09724676

GENERAL INFORMATION:
APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UNMBER: US/09/724,676

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 93256

LENGTH: 430

TYPE: PRT

ORGANIAM: Homo sapiens
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US-09-724-676-93256
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                             ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-724-676-93267
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                                                                             SOFTWARE: PatentIn version 3.2
SEQ ID NO 93267
LENGTH: 430
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Query Match
                                                                                                                         APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION NUMBER: US/09/724,676 CURRENT FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 97222
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99.6%;
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Score 2000;
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative sp
TITLE OF INVENTION: Variants of alternative sp
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SEQ ID NO 93278
SEQ ID NO 93278
LENGTH: 430
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US-09-724-676-93278
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Best Local Similarity
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            PERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLJTRHAVV
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PERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVV
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                                                                                                                                   FERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLK
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; Pred. No. 4e-1
1; Mismatches
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1; Mismatches
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Sequence 93300, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative sp.
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UNMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTMARE: Patentin version 3.2
SEG ID NO 93300
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; TITLE OF INVENTION: Variants of alternative sp
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676;
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93289
; LENGTH: 430
; TYPE: PRT
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US-09-724-676-93300
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Sequence 93289, Application US/09724676

GENERAL INFORMATION:
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US-09-724-676-93289
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LENGTH: 430
TYPE: PRT
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Pred. No. 4e-176;
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GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative sp
FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 93212
                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens US-09-724-676A-93212
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Best Local :
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TYPE: PRT
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Pred. No. 46
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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative sp
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 93223
SEQ ID NO 93223
LENGTH: 430
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            Sequence 93234, Application US/09724676A GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION UNMBER: US/09/724,676A CURRENT FILING DATE: 2000-11-28
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Matches
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NUMBER OF SEQ ID NOS:
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US-09-724-676A-93245
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TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 93245
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Best Local Similarity
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SEQ ID NO 93234
LENGTH: 430
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Sequence 93256, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative sp
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UNMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEO ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEO ID NO 93256
RESULT 15
US-09-724-676A-93267
; Sequence 93267, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-93256
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Search completed: February 10, Job time: 42 secs

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CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEO ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEO ID NO 93267
LENGTH: 430
TYPE: PRT
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Best Local
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VLTLG
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Copyright (c) 1993 - 2003
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                        AAY93317
AAG75181
AAR91305
ABP41846
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Compugen Ltd
Human protein :
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Amino acid sequenc
Novel human diagno
Human protein SEQ
Human protein SEQ
Human protein SEQ
Human protein SEQ
                                                                                                                                                                                                                                                        Description
                                                                                                                                                            A human transcript
Human colon cancer
Transcription fact
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613	386	357	1520	577	406	759	1252	817	632	570	547	799	702	489	751	809	727	803	1050	412	577	646	773	934	779	779	779	1241	700	403	652	632	631	622
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AAB95862	w	AAB93635	ABG27130	AAE14680	AAU16023	AAU78844	AAM79739	AAM40475	ABG19011	AAM79350	AAM78366	AAB21003	ABB04333	ABB50238	AAM39508	AAM38689	ABG16954	AAB95278	ABG09685	AAY93316	AAM93698	ABP51377	AAM41294	ABB69958	ААМ79958	AAM78974	ABG00880	ABG02797	AAM40001	ABB64531	AAM79171	ABG18386	AAM79931	AAM78947 .
Human protein sequ	epi	Human protein sequ	Novel human diagno	Human transcriptio	Human novel secret	SCAN/KRA	Human protein SEQ	Human polypeptide	. human di	Human protein SEQ	Human protein SEQ	Human nucleic acid	Human zinc finger	Human transcriptio	Human polypeptide	Human polypeptide	Novel human diagno		Novel human diagno	A transcription fa	Human polypeptide,	Human MDDT SEQ ID	Human polypeptide	Drosophila melanog		Human protein SEQ	Novel human diagno	Novel human diagno	Human polypeptide	Drosophila melanog	n proteir	₩.	protein	Human protein SEQ

## ALIGNMENTS

RESULT 1
AAY93317
ID AAY9

AAY93317 standard; Protein; 365 AA

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New nucleic acid encoding human transcription factor IIIA, useful for treatment and diagnosis of cancer and inherited disease
                        WPI; 2000-387419/33.
N-PSDB; AAA15405.
                                                                                                09-NOV-1999;
                                                                                                                                               Homo sapiens.
                                                                                                                                                               cancer.
                                               Bordon-Pallier F,
                                                                                                                18-MAY-2000
                                                                                                                               WO200028024-A1
                                                               (HMRI ) HOECHST MARION ROUSSEL
                                                                                10-NOV-1998;
                                                                               98FR-0014146.
                                                                                               99WO-FR02738
                                               Rocher C;
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Human; transcription factor; htfIIIA; DNA-binding protein; transcription; ribosomal RNA 5S gene; transcriptional control;

A human transcription factor designated htfIIIA.

04-SEP-2000 AAY93317;

(first entry)

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RESULT 2
AAG75181
ID AAG7
AC AAG7
AC AAG7
XX
AC AAG7
XX
BE Huma
XX
BE Homo
XX
COLO
XX
HOmo
XX
HOmo
XX
PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                               Human colon cancer antigen protein SEQ ID NO:5945
                                                                                                                                                                                                                                                                 03-SEP-2001
                                                                                                                                                                                                                                                                                                                           AAG75181 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                03-NOV-1999;
                               29-SEP-1999;
                                                              28-SEP-2000; 2000WO-US26524
                                                                                                                          WO200122920-A2
                                                                                                                                                                                     colorectal carcinoma;
                                                                                                                                                                                                   Human; colon cancer; colon cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                                                       361
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Pred. No. 2.5e-159;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                  AAR91305
                                                  AAR91305 standard;
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Pred. No. 1.4e-158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 8-10; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Transcription Factor III A gene - useful in regulation
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                                                       HDPDKKKMKLKVKKSREKRSLASHLSGYIPPKRKQGQGLSLCQNGESPNCVEDKMLSTVA
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Pred. No. 5.5e-153;
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The invention relates to 2175 novel human ovarian antigens (ABP41054-CC ABP43228) and to cDNAs encoding them (ABC54311-ABC56305), and also cencompasses polypeptides 90% identical and polypnucleotides 95% identical ct to the sequences of the invention. The invention additionally relates to crecombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use cf of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related ct treating, prognosing or preventing various ovary and/or breast-related ct disorders. Such conditions include ovarian cancer and breast cancer, and cancer disorders. (e.g., infertility, disorders of pregnancy, anovulation, copolycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine ct disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and cysts, and dysmenorrhoea), and toxic shock syndromes, autoimmune ophoritis, systemic lupus erythematosus), blood-related disorders (e.g., canamia), cardiovascular disorders (e.g., material), cardiovascular disorders cand urinary system disorders. Ovarian antigen polypeptides and condulate ovarian antigen sursession or activity. The polynucleotides may also be used in screening for compounds which compounds condulate ovarian antigen expression or activity. The polynucleotides may crement of the compounds which condulate ovarian antigen expression or activity. The polynucleotides may crement of the compounds which condulates and conductive ovarian antigen expression or activity. The polynucleotides may crement condulates and conductive ovarian antigen expression or activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndron PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; incorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antibody preparation; cytostatic; immunomodulatory; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; SEQ ID No 2978; 2922pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABQ54923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiinflammatory; gynaecological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ovarian antigen HUSYA18,
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RESULT 5
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Matches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
rne invention relates to a nucleic acid (NA) binding comprising a repressor domain and several NA binding by at least one non-canonical linker. (I) may be used a complex mixture, to differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                          Nucleic acid binding polypeptide, used to identify nucleic acids and treat inflammatory, neurological, and dermatological disease, compris a repressor domain and several nucleic acid binding domains linked by
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid binding polypeptide; repressor domain; cardiant; nootropic circulatory active; anti-inflammatory; dermatological; neuroprotective; cerebroprotective; anti-bacterial; antifungal; antiviral; antirheumatic;
                                                                    Claim 31; Fig
                                                                                                 non-canonical
                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                   24-JAN-2000; 2000GB-0001582; 30-MAY-2000; 2000GB-0013102; 30-MAY-2000; 2000GB-0013103; 30-MAY-2000; 2000GB-0013104
                                                                                                                                                                                                                                                                                                                                                                                            WO200153480-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    osteopathic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB85422 standard;
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                                                                                                                                                                                                                                                                                                                                                                   26-JUL-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGCSFVAKTWTELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPREG 252
                                                                                                                                                                    2001-451906/48.
DB; AAH23370.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRMSLCGKTWADLLXHVREPIKREXLCGVCRKTFNAKDYLKQPMKTHAPERDVCRCPREG
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                                                                                                                                                                                                             Klug A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; zinc finger; binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                   15; 142pp;
                                                                                               linker(s)
                                                                                                                                                                                                              Moore
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89.6%;
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                                                                    English
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Pred. No. 1.1e-6
1; Mismatches
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1. No. 1.1e-60;
17;
             (I) may be used to identify NAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain; cardiant; nootropic;
pair changes in NAs,
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                          polypeptide (domains (BDs)
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organisms, and in the treatment of diseases such as: cardiovascular, inflammatory, metabolic, infectious, neurological, rheumatological, genetic, dermatological, and musculoskeletal diseases. The invented methods are used to produce novel NA binding polynucleotides and to modify existing was binding polynucleotides comprising several NA BDS. The novel polypeptide comprises several nucleic acid binding domains linked by linker sequences. The invented polypeptide is therefore able to span longer or variable gaps, and a greater number of gaps, between DNA binding subsites. The present sequence represents the amino acid sequence of TFIIIA(FI-4)-ZIF fusion zinc finger construct.
New isolated polynucleotide and encoded polypeptides, us diagnostics, forensics, gene mapping, identification of responsible for genetic disorders or other traits and to
                                                                                                                                                                      31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                11-OCT-2001.
                                                                                                                                                                                                                                                                              WO200175067-A2
                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy;
food supplement; medical imaging; diagnostic; genetic of
food supplement; medical imaging; diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                    Novel human diagnostic protein #9338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG09347
                                                                                                                                                                                                                                                                                                                                       food supplement; medical imaging;
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                                                                             2001-639362/73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRPFVCEHAGCGKTFAMKQSLTRHAVVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQKGCSFVAKTWTELLKHVRETH 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTGEKNFTCDSDGCDLRFTTKANMKKHFNRFHNIKICVYVCHFENCGKAFKKHNQLKVHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTGEKPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVVYKRYICSFADCGAAYNKNWKLQAHLCKHTGEKPFPCKEEGCEKGFTSLHHLTRHSLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103;
                                                              AAS73534
                                                                                                                                        HYSEQ
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                                                                                                           RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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                                                                                                         Liu
                                                                                                                                                                      2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                   (first
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                                                                                                                                                                                                                                                                                                                                                                                                                   entry;
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 gene mapping, identification of mutatio disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                         genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                  mutations
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RESULT 7
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Best Local :
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                                        03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensies, gene mapping, identification of mutations are responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromo and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                        WO200157190-A2
                                                                                                                                                                                                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
                                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM80283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM80283 standard; Protein;
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                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                       nervous system disorder; arthritis; inflammation
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                                                                                             AAM79299 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy \cdot
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N-PSDB; AAK53416.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIHTGERPNTC -- SECGKSFTQSSHLVQHQRTHTGEKPYKCPDCGKCFSWSSNLVQHQRT 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPAVVAESVSSLTIADAFIAAGESSAPTPPRPA-LPRRFICSFPDCSANYSKAWKLDAHL 61
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                                                                                              Protein; 869
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Pred. No.
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No. 9.1e-27;
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Ren F, C
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Human protein SEQ ID NO 1961

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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
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Zhao
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                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; Page 4372-4374; 6221pp; English
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                             156
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116; Conser
HTGEKPYKCPE--CGKRFGQNHNLLKHQKIHAGEKPYRCTECGKSFIQSSELTQHQRTHT
                             HTNEPLEKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQK-GCSFV-----AKTWT
                                                       HTGEEPYKCTECEIAFTQSTNLIKH-QRSHTG-EKPYKCG--ECRRAFYRSSDLIQHQAT 283
                                                                        -----AATGCDOKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQ 155
                                                                                                              RIHTGERPNTC--SECGKSFTQSSHLVQHQRTHTGEKPYKCPDCGKCFSWSSNLVQHQRT 227
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DB; AAK52432.
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2000US-0560875.
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Wejhrman T,
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                                                                                                                                                                                                                             Score 421; DB 22;
Pred. No. 1.8e-26;
1; Mismatches 116
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
                                                                                     The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78233-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of carcio activity and may be useful in the diagnosis and/or treatment of carcio activity and may be useful in the diagnosis and/or treatment of carcio activity and may be useful in the diagnosis and/or treatment of carcio activity and may be useful in the diagnosis and/or treatment of carcio activity and may be useful in the diagnosis and/or treatment of the carcio activity and activity activity and activity and activity and activity and activity and activity activity activity and activity activity and activity activity activity activity activity and activity activi
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15-SEP-2000;
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                                                                                                                                                                                                                                                                                                                     Claim 20; Page 4019-4021; 6221pp; English.
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Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing
                                                inflammation.
                                                                         treatment of cancer, leukaemia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2001
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DB; AAK52147.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C, Drmanac RT, Wang D, Wang J, Z: Yang Y, Wejhrman T,
                                                                                                                                                                                                                                                                                                                                                                      diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0496914.
2000US-0560075.
2000US-0598075.
2000US-0620325.
2000US-063936.
2000US-0639315.
2000US-0633325.
2000US-0728422.
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                                                                                                                                                                                                                                                                                                                                                                    gene
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, Zhang J, Ren
n T, Goodrich R
                                                                                                                                                                                                                                                                                                                                                                 therapy
                                                                      nervous system disorders,
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F, (
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ing ZW;
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         Tang
Zhao
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                                                                                                                                                                                                                                                      Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; pervous system disorder; arthritis; inflammation.
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27-APR-2000;
                                                                                                                                                                                                                                                                                                              Human protein
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19-JUL-2000;
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                                         (HYSE-) HYSEQ INC
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20-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DAFTAAGESSAPTP------PRPALPRR-----FICSFPDCSANYSKAWKLD 58
        QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVVH--DPDKKKMKLKV----KKSRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DILLAEPAEPAPAPAPEEEAEGPAAALGPRGPLGSGPGVVLYLCPEAQCGQTFAKKHQLK 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRSLASHLSGYIPPKRKQGQGL 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLLRH------KRK-----HDDDRRF-MCPVEGCGKSFTRAEHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                      KHSMKTHM----VKRHKVGQDL 578
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        Liu C,
Wang D,
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2000US-0560875.

2000US-0598075.

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2000US-064936.

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2000US-0693325.

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2000US-0728422.
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       Drmanac RT, Asundi V,
Wang J, Zhang J, Ren
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        Zhou
F, C
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RESULT 11
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Best Local :
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Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; Page 404-405; 6221pp; English.
                                                               Human protein
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                                                                                                06-NOV-2001
                                                                                                                                                               AAM78947 standard;
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DB; AAK53131.
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Pred. No. 6.6e-26;
7; Mismatches 131
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Best Local S
Matches 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to polynucleotides (AAKS1456-AAKS3435) and the encoded polypeptides (AAK9333-AAK80302) that exhibit activity elating to cytokine, cell poliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, heemstopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
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Zhao QA,
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27-APR-2000;
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19-JUL-2000;
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20-OCT-2000;
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C--EECGKAFVASSTLSKHEI-IHTGKKPYKCEE--CGKAFNQSSSLTKHKKIHTGEKPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YKCEECGKAFNQSSTLTKHKKIHTGEKPYKCEECGKAFNQSSTLTKH--KKIHTGEKPYV 316
                                                                                           CPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKK-
                                                                                                                                                                                      CEECGKAFI---WSSVLTRHKRVHTGEKPYKCEECGKAFKYSSTLSSHKRSHTGEKPY-K 428
                                                                                                                                                                                                                                                   CQK-GCSFVAKTWTELLKHVRETHKEE--ILCEVCRKTFKRKDYLKQHMKTHAPERDVCR
                                                                                                                                                                                                                                                                                                                                                                        C--EECGKAFKYSRILTTHKRIHTGEKPYKCNK--CGKAFIASSTLSRHEFIHMGKKHYK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEG---YV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YICE--ECGKAFKYSSALNTHKRIHTGEKPYKCD--KCDKAFIASSTLSKHEIIHTGKKP
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Wang D, Wang J, zl
Yang Y, Wejhrman T,
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pred. No. 8.9e-26;
48; Mismatches 137;
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from
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the sequence listing
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R, Wang
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Query Match Best Local S Matches 109

Local Similarity mes 109; Conserv

Conservative

30.5%;

b; Score 410.5; b; Pred. No. 9.16 48; Mismatches

9.1e-26; DB 22;

Length 631;

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Gaps

17

Mismatches

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19-JUL-2000;
01-SEP-2000;
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Zhao QA,
Xue AJ,
                                                                                                                                                                                          The invention relates to polynucleotides (AAK53435, AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hematopolesis regulating
                                                                                                                            activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and treatment of cancer, leukaemia, nervous system disorders, arthritis and treatment of cancer, leukaemia, nervous system disorders, arthritis and treatment of cancer, leukaemia, nervous system disorders, arthritis and treatment of cancer, leukaemia, nervous system disorders, arthritis and treatment of cancer, leukaemia, nervous system disorders, arthritis and treatment of cancer, leukaemia, nervous system disorders, arthritis and treatment of cancer, leukaemia, nervous system disorders, arthritis and treatment of cancer, leukaemia, nervous system disorders, arthritis and treatment of cancer, leukaemia, nervous system disorders, arthritis and treatment of cancer, leukaemia, nervous system disorders, arthritis and treatment of cancer, leukaemia, nervous system disorders, arthritis and treatment of cancer, leukaemia, nervous system disorders, arthritis and treatment of cancer, leukaemia, nervous system disorders, arthritis and treatment of cancer, leukaemia, nervous system disorders, arthritis and treatment of cancer, leukaemia, nervous system disorders, arthritis and treatment of cancer.
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                                      Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAM80020) are omitted as the relevant pages from were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Page 388; 6221pp; English
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N-PSDB; AAK53064.
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27-APR-2000;
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Yang Y,
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2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
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Wejhrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT, Asundi V, zhou P, Wang J, Zhang J, Ren F, Cher Wejhrman T, Goodrich R;
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                                                                                                                              nervous system disorders, arthritis and
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                                                              (AAK52582) and 3666
the sequence listing
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R, Wang
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in acciding
                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                     Claim 20; SEQ ID No 48745; 103pp; English.
                                                                                                                                                                                                                                                                                                              N-PSDB;
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RESULT 14
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Best Local
03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printer specification, but was obtained in electronic format directly from W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                       Human; cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                       AAM79171;
                                                                                                                              05-FEB-2001;
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                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                         nervous system disorder; arthritis; inflammation
                                                                                                                                                                                                                                                                                                                                       Human protein
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2000US-0496914.
2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
2000US-0663561.
2000US-0693325.
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Pred. No. 9.1e-26;
8; Mismatches 13;
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Zhao
                                                                                  \label{eq:decomposition} \begin{picture}(100,00) \put(0,0){\line(0,0){100}} \put(0,0){\line(0,0){1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78333-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The prolynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hematopolesis regulating.
                            Drosophila melanogaster
                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ
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                                                                                                                                                                                                                                                                                                                                                        ABB64531 standard; Protein;
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6 QA,
7 YY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E--CGKAFNWSSSLTKHKIIHTGEK 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAGCGKTFAMKQSLTRHAVVHDPDK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEGCGKHFASPSKLKRHAKAHEG---YVCQKGCSFVAKTWTELLKHVRETHKEEIL--CE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCT 165
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DB; AAK52304.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECGKAFTRSTALNEHKKIHSGEKPY-KC--KECGKAYNLSSTLTKH-KRIHTGEKPFTCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -CGKAFNQSSTLILH-KRIHSG-QKPYKC--EECGKAFTRSTTLNEHKKIHTGEKPYKC- 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ECGKAFTWSSSLNKHKRIHTGEKPYTC -- EECGKAFYRSSHLAKHKRIHTGEKPYTCEE- 431
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Wang D, Wang J, Zhang J, Ren
Yang Y, Wejhrman T, Goodrich R,
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Pred. No. 9.5e-26;
1; Mismatches 111
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Matches 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABU30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid genes from Drosophila and interactions .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 20385; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US09231
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mes 105; Conserv
                             KRSLASHLSGYIPPKRKQGQGLSLCQNGESPNCVEDKMLSTVAVLTL 364
                                                                                                                                                                                          EIREHTLEYPYSCSK--CSRGFYQQWQCQSHEPSCKLYEC-PGCPLQFDKWTLYTKHCRD
                                                                                                                                                                                                                                                                                                                        KYACSMPKCEATFKRLDQLDRHEYHHTGIKKHACSYEGCDKTYSIVTHLKRHLRSTHERP 93
                                                             YLRNLRQHMLTAH-SGRRFECQALDCGRCFSSAQNLARHLLRDHKDGATKKELKAKKKDK
                                                                                          TVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAV-VHDPDKKKMKLKVKKSRE
                                                                                                                            SLHGKNRHK----CDRCDSAFDKPSELKRHLEVKHKEAAQTDECATSFTCNEEGCGKSYS
                                                                                                                                                           T-----HKEEILCEVCRKTFKRKDYLKQHMKT---HAPERDVC----RCPREGCGRTYT
                                                                                                                                                                                                                          QC-QHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQKGCSFVAKTWTELLKHVRE
                                                                                                                                                                                                                                                         ESAAKKTVKCALEECSKMFISVSNMTRHMRETHES-PKVYPCS--QCSAKFSQKLKLKRH
                                                                                                                                                                                                                                                                                         --TGEKPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIH 152
                                                                                                                                                                                                                                                                                                                                                        RFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHI-LTH---
SKTGEGGKTKSTSRKRRRDAGRS-----KHSRLSKLACLQL
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Pred. No. 1.1e-25;
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Search completed: February 10, Job time: 77 secs

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1: /cgn2_6/pcodata/1.

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US-09-565-538-10
US-09-661-468-10
US-09-661-468-10
US-09-663-035-2
US-08-475-844-9
PCT-US95-08429-9
US-08-486-099-117
US-08-486-099-117
US-08-486-099-117
US-08-486-5264-117
US-08-486-5264-117
US-08-471-349A-117
US-08-471-349A-117
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US-08-475-08429-5
PCT-US9-08-495-51A-117
US-08-476-378A-17
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US-08-676-378A-44
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APPLICANT: TSULOMA, FUJIWARA
APPLICANT: Satoshi, TAKEDA
APPLICANT: Yoshikazu, SHIMAD
APPLICANT: Kouichi, OZAKI
APPLICANT: Sadahito, SIN
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                                                                                                                                                                                                                                 Query Match
Best Local S
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INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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LENGTH: 423 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEPHAX: (202) 293-7860
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STREET: 2100 Pennsylvan.
CITY: Washington
STATE: D.C.
COUNTRY: United States
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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Sadahito, SIN
SENTION: hTFIIIA GENE
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Pred. No. 8.3e
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Best Local S
Matches 93
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 293-7060
TELEPHONE: (202) 293-7860
TELEFAX: (202) 293-7860
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CORRESPONDENCE ADDRESS:
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APPLICANT: Masato, HORIE
APPLICANT: Toyomasa, KATAGIRI
TITLE OF TAVERMETON: ......
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APPLICANT:
501 KPYEC--SDCGKTFTQKSHLNIH--QKIHTGERHHVCS--ECGKAFNQKSILSMHQRIHT
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                                                                                 445 KSYVCI--ECGQAFIQKAHLIVHQRSHTGEKPYQC--HNCGKSFISKSQLDIHHRIHTGE 500
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                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 536
                                           98 KPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHT 157
                                                                                                                     38 RRFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGE 97
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-055-699-10
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENCTH: 711 amino
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APPLICANT:
APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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214 KEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPRE--GCGRTYTTVFNLQSHILSFH 271
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                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
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TELEFAX: (202) 293-7860
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                                                                                                             KPYEC--SDCGKTFTQKSHLNIH--QKIHTGERHHVCS--ECGKAFNQKSILSMHQRIHT 554
                                    GEKPYKCSE--CGKAFTSKSQFKEHQRIHTGEKPYVCTE-CGKAFNGRSNFHKHQITHTR
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Masato, HORIE
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Pred. No. 2.6e-30;
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 711
TYPE: PRT
ORGANISM: Homo saplens
US-09-273-565-10
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EARLIER APPLICATION NUMBER: 09/05/69
EARLIER APPLICATION NUMBER: 09/05/69
EARLIER APPLICATION NUMBER: 09/05/69
EARLIER FILING DATE: 1998-04-07
EARLIER FILING DATE: 1997-03-19
EARLIER FILING DATE: 1996-03-19
EARLIER FILING DATE: 1996-03-19
EARLIER FILING DATE: 1996-03-19
EARLIER APPLICATION NUMBER: JP 69163/1997
EARLIER APPLICATION NUMBER: JP 69163/1997
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             GENERAL INFORMATION:
APPLICANT: FUJIWARA, TSUTOMU
APPLICANT: WATANABE, TAKESHI
APPLICANT: HORIE, MASATO
TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING E
                                                                                                                                                                          Sequence 10, Application US/09565538 Patent No. 6333404
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Best Local Similarity
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FILE REFERENCE: Q-53599
                                                                                                                                                                                                                                                                                                                     666 TGERPYVCSE--CGKAFNNRSNFNKHQTTHTRDKSYKCSYSVK 706
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; ORGANISM: Homo sapiens
US-09-661-468-10
                                                                                                                                                    CURRENT APLICATION NUMBER: US/09/661,468
CURRENT FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 09/055,699
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: 08/820,170
PRIOR FILING DATE: 1997-03-19
PRIOR APPLICATION NUMBER: JP 63410/1996
PRIOR APPLICATION NUMBER: JP 6963/1997
PRIOR FILING DATE: 1997-03-05
PRIOR APPLICATION NUMBER: JP 69163/1997
PRIOR FILING DATE: 1997-03-05
PRIOR APPLICATION NUMBER: JP 69163/1997
PRIOR FILING DATE: 1997-03-05
                                                                                     SOFTWARE: I
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Patent No. 6376189
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PRIOR FILING DATE: 1997-03-19
PRIOR APPLICATION NUMBER: JP 63410/1996
PRIOR FILING DATE: 1996-03-19
PRIOR APPLICATION NUMBER: JP 69163/1997
PRIOR FILING DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 95
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PRIOR FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: 09/055,699
PRIOR FILING DATE: 1998-04-07
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CURRENT FILING DATE: 2000-05-05
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                                                                                                                                     NUMBER OF SEQ ID NOS:
                                          LENGTH: 711
TYPE: PRT
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SEQ ID NO 4
LENGTH: 543
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APPLICANT: Sirenko, Okaana
TITLE OF INVENTION: NO. 6451558el Genes in
TOTALE OF TRYENTON: NO. 6451558el Genes in
TOTALE OF TRYENTON: NO. 6451558el Genes in
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/362,123A CURRENT FILING DATE: 1999-07-27 PRIOR APPLICATION NUMBER: 09/128,310 PRIOR FILING DATE: 1998-08-03 NUMBER OF SEQ ID NOS: 7 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                          54
                                                                                                                                                                                     340
                                                                                                                                                                                                                        143
                                                                                                                                                                                                                                                                                                                           242 AGEKS-----FECR--ACSKVFVKSSDLLKHLRTHTGERPYEC--AQCGKAFS 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 KEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPRE--GCGRTYTTVFNLQSHILSFH 271
                                                                                                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                              23 AGESSAPTPPRPALPRRFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGGGKAFI 82
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     RSLASHLSGYIPPKRKQ 335
                                      KGAVLLSH-RRIHTGEKPFVCTQ--CGRAFRERPALFHHQRIHTGEKTVRRSRASLHPQA 510
                                                                       TVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKSREK 318
                                                                                                            SQGSSLFKHQRVHTGEKPFACPQCGRAFSHSSNLTQHQLLHTGERPF-RC--VDCGKAFA 453
                                                                                                                                               KTWTELLKHVR-ETHKEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYT 258
                                                                                                                                                                                  FSHGSNLSQHRKIHAGGRPYACAQ--CGRRFCRNSHLIQHERTHTGEKPFVCAL-CGAAF 396
                                                                                                                                                                                                                    FKKHOOLKIHOCOHTNEPLFKCTOEGCGKHFASPSKLKRHAKAHEG---YVCOKGCSFVA 199
                                                                                                                                                                                                                                                       TSHLTQHQRIHSGETPYACPV--CGKAFRHSSSLVRH-QRIH-TAEKSFRCS--ECGKA 339
                                                                                                                                                                                                                                                                                        RDYHLSRHILTHTGEKPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGERPYVCSE--CGKAFNNRSNFNKHQTTHTRDKSYKCSYSVK 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKK-KMKLKVK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERPFVCYKCGKAFVQKSELITHQRTHMGEK-----PYECLDCGKSFSKKPQLKVH-QRIH 665
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                                                                                                                                                                                                                                                                                                                                                                                                                    17.6%; Score 353.5; DB 4; Length 543; 31.5%; Pred. No. 1.2e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                     38; Mismatches 144; Indels
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TOPOLOGY: linear
US-09-063-035-2
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                                                                                       APPLICANT: Lobane
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INFORMATION FOR SEQ ID NO:
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                   APPLICANT:
                                                    APPLICANT:
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LENGTH: 803 amino acid
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APPLICATION NUMBER: US,
FILING DATE: 21-APR-19
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APPLICANT:
 APPLICANT:
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CITY: Washington
STATE: D.C.
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les 95; Conserv
Klenova, Elena M.
Goodwin, Graham H.
Filippova, Galina N.
Collins, Steven J.
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Martin
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Sequence 9, Application US/08475844 Patent No. 5972643
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ZIP: 20036
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.2 Mb storage
COMPUTER: IBM AT-compatible, 80486 processor
OPERATING SYSTEM MS-DOS version 6.1
COFTWARE: WordPerfect version 8.0
COFTWARE: MORDER DATA:
                                                                                                                                                                                                                                                                                  509 RQFADPGALQRHVRIHTGEKPCQCVMCGKAFTQASSLIAHV-----RQHTGEKPYVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344 SDPAACKAH-EKTH-SPLKPYGC--EECGKSYRLISLLNLHKKRHSGEARYRC--EDCGK 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 SKAYGSVIHKC------EDCGKEFTHTGNFKRHIRIHTGEKPFSCRE--CSKAF 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HFASPSKLKRHAKAHEG---YVCQKGCSFVAKTWTELLKHVRETH--KEEILCEVCRKTF 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCTQEGCGK 171
                                                                                                                                                                                                                                                                                                                                                                                                          NQVGNLKAHLKIHIADGPLKCR----ECGKQFTTSGNLKRQ-LRIHSGEKPYVCIH--CQ 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFTTSGNLKRHQLVHSGEKPYQCDY-CGRSFSDPTSKMRHL-ETHDTDKEHKCPHCDKKF 455
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Neiman, Paul E.
                                 Lobanenkov, Victor V.
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21-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.7%; Score 336; DB 4; Length 803; 31.8%; Pred. No. 1.2e-25; tive 45; Mismatches 117; Indels
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Sequence 9, Application PC/TUS9508429
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 206-467-9600 TELEFAX: 415-543-5043
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LENGTH: 727 amino acids
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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STATE: C
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Parmelee, Steven W. REGISTRATION NUMBER: 31,990 REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/475,844 FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 PPRP------ALPRRFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRD 84
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                                                                                        RKRKMRSKKEDSS 610
                                                                                                                           KYKKSREKRSLAS 323
                                                                                                                                                              MHFKRYHDPNFVPAAFVC--SKCGKTFTRRNTMARHADNCAGPDGVEGENGGETKKSKRG 597
                                                                                                                                                                                             SHILSFHEES---RPFVCEHAGCGKTFAMKQSLTRHA-VVHDPD------KKKMKL 310
                                                                                                                                                                                                                                  YALIQHQKSHKNEKRFKCDQCDYACRQERHMIMHKRTHTGEKPYACSHCDKTFRQKQLLD 539
                                                                                                                                                                                                                                                                      GTMKMHILQKHTENVAKFHCPHCDTVIARKSDLGVHLRKQHSYIEQGKKCRYCDAVFHER 479
                                                                                                                                                                                                                                                                                                                                                                                 EVSKLKRHIRSHTGERPFQCSL--CSYASRDTYKLKRHMRTHSGEKPYECYICHARFTQS 419
                                                                                                                                                                                                                                                                                                                                                                                                                   KHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEG-----YVC-----QK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLLRNHLNTHTGTRPHKC -- PDCDMAFVTSGELVRHRRYKH-THEKPFKCSM--CDYASV 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YHLSRHILTHTGEKPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPKPTKIKKKGVKKTFQCEL--CSYTCPRRSNLDRHMKSHTDERPHKCHL--CGRAFRTV 300
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                                        US-09-262-773-4
                                                         RESULT 11
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Sequence 4, Application US/09262773 Patent No. 6225451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 727 amino acids
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PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/261,680
FILING DATE: 17-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
TITLE OF INVENTION:
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                                                                                                                   598 RKRKMRSKKEDSS 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14538A-11-1PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 PPRP-----ALPRRFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                MHFKRYHDPNFVPAAFVC--SKCGKTFTRRNTMARHADNCAGPDGVEGENGGETKKSKRG 597
                                                                                                                                                                                                                                    SHILSFHEES----RPFVCEHAGCGKTFAMKQSLTRHA-VVHDPD------KKKMKL 310
                                                                                                                                                                                                                                                                           YALIQHQKSHKNEKRFKCDQCDYACRQERHMIMHKRTHTGEKPYACSHCDKTFRQKQLLD 539
                                                                                                                                                                                                                                                                                                                 GTMKMHILQKHTENVAKFHCPHCDTVIARKSDLGVHLRKQHSYIEQGKKCRYCDAVFHER 479
                                                                                                                                                                                                                                                                                                                                                                                              G-----KEEILCEVCRKTFKRK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                    EVSKLKRHIRSHTGERPFQCSL··CSYASRDTYKLKRHMRTHSGEKPYECYICHARFTQS 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEG-----YVC-----QK 193
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27.6%;
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GENERAL INFORMATION:
APPLICANT: Ballinger,
APPLICANT: Ding, Wei

APPLICANT: Wagner, Susanne

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APPLICANT: Ding, Wei
APPLICANT: Hess, Mark A.
APPLICANT: Hess, Mark A.
APPLICANT: Hess, Mark A.
TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE
TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
FILE REFERENCE: Myr1ad 3
CURRENT APPLICATION UNMBER: US/09/262,773
CURRENT FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 210
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 648
TYPE: PRT
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; ORGANISM: human
US-09-262-773-4
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US-09-262-773-2
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                                                                                  Best Loc
Matches
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TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE
TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1

FILE REFERENCE: MY 11ad 3

CURRENT APPLICATION NUMBER: US/09/262,773

CURRENT FILLING DATE: 1998-03-04

NUMBER OF SED ID NOS: 210

SOFTWARE: Patentin Ver. 2.0

SED ID NO 4

LENGTH: 640
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APPLICANT: Ballinger,
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                                          SSLTIADAFIAAGESSAPTPPRPALPRRFICSFPDCSANYSKAWKLDAHLCKHTGERPFV 71
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                                                                                    Conservative
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                                                                             15.6%; Score 313; DB 4
31.6%; Pred. NO. 2e-23;
tive 44; Mismatches 1
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Pred. No. 1.9e-23;
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                                                                                                                        DB 4; Length 648;
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; TOPOLOGY: unknown ; MOLECULE TYPE: protein US-08-486-099-117
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Query Match 15.6
Best Local Similarity 32.9
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                               APPLICATION NUMBER: U5/08/486, FILING DATE: 07-JUN-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: COTUZZI, LBUITA A. REGISTRATION UMBER: 30,742 REFERENCE/DOCKET NUMBER: 7872-TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9990 TELEPHONE: (212) 869-9741/8864
                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Petteway, Stephen R.
APPLICANT: Langiois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
TITLE OF INVENTION: B VIRUS TRANSMISSION
                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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TELEFAX: 66141
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TYPE: a
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CITY: 1
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                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSVEKPYRC -- DDCGKHFRWTSDLVRHQRTHTGEKPFFCTI -- CGKSFSQKSVLTTHQRI 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
                                                                                                                                                       amino acid
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                                                                                                                                                                     462 amino acids
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1155 Avenue of the Americas
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                      15.6%;
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    35;
  Score 312.5; DB 3;
Pred. No. 1.4e-23;
35; Mismatches 101;
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                                        Length 462;
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                                                               ; TOPOLOGY: unknown ; MOLECULE TYPE: protein US-08-360-107A-127
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US-08-360-107A-127
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                         NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-(
TELECONMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Langlois, Alphonse J.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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  15.6%;
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  Score 312.5; DB 3; Pred. No. 1.4e-23;
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                        Length 462;
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; TOPOLOGY: ui
; MOLECULE TYPE:
US-08-484-223B-117
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US-08-484-223B-117
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 Query Match
                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9990
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Bologn
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TITLE OF INVENTION: OF
TITLE OF INVENTION: N
                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                TYPE: amino
STRANDEDNESS:
                                                                                                                                                                                                                                      NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 07-JUN
                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                    amino acid
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                                                                                                                    462 amino acids
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Langlois, Alphonse J.
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Lambert, Dennis M.
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                                                                   unknown
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 15.6%;
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 Score 312.5;
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Length 462;
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Search completed: February 10, 2003, 17:48:58 Job time: 28 secs
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                                                                                                                             389 RKNDLIKHQRIH 400
                                             290 MKQSLTRHAVVH 301
                                                               341 QRTHTGEK-----PYECHDCGKSFS-----QSSALIVHQRIHTGEKPYEC--CQCGKAFI 388
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Result
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Maximum DB
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    and is derived by analysis of the total score distribution.
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  385
383.5
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1: /cgn2_6/ptcodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptcodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptcodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptcodata/1/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptcodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptcodata/1/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_6/ptcodata/1/pubpaa/US09_PUBCOMB.pep:*

9: /cgn2_6/ptcodata/1/pubpaa/US09_PUBCOMB.pep:*

9: /cgn2_6/ptcodata/1/pubpaa/US09_NEW_PUB.pep:*

10: /cgn2_6/ptcodata/1/pubpaa/US09_NEW_PUB.pep:*

11: /cgn2_6/ptcodata/1/pubpaa/US10_NEW_PUB.pep:*

12: /cgn2_6/ptcodata/1/pubpaa/US10_NEW_PUB.pep:*

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14: /cgn2_6/ptcodata/1/pubpaa/US10_NEW_PUB.pep:*
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          Sequence 30, Appl
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Sequence 212, App
Sequence 1357, Ap
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16.1	16.1	16.2	16.2	16.3	16.5	16.5	16.5	16.6	16.8	17.0	17.1	17.1	17.1	17.1	17.3	17.3	17.4	17.4	17.5	17.6	17.6	17.7	17.7	17.7	17.7
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		Sequence 1		Sequence 3			Sequence 9	Sequence 1																	Sequence 9
37026, A	7994, A	.076, Ap	6336, A	33477, A		883, App	958, App	2, Appl	37010, A	34333, A		940, App	893, App	•	1063, Ap		932, App	887, App	37651, A		33476, A	37943, A	6132, A	97	935, App

## ALIGNMENTS

US-09-764-864-976 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 976 LENGTH: 406 TYPE: PRT Sequence 976, Application US/09764864 Patent No. US20020132753A1 GENERAL INFORMATION: Query Match Best Local : Matches APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REPERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17 Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792 ORGANISM: Homo sapiens 302 247 223 190 134 107 283 167 82 47 CSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAATG 106 Local Similarity GCGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKS-REKRSLASHLSGYIPPKRKQGQGLSL 341 GKAFGQKSQLRGHHRIHTGEKPY-KC--NHCGEAFSQKSNLRVHHRT-HTGEKPYQCEE- 301 RKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHA 282 EGCGKHFASPSKLKRHAKAHEG---YVCQKGCSFVAKTWTELLKHVR-ETHKEEILCEVC CDKAFSAKSGLRIH-QRTHTG-EKPFEC--HECGKSFNYKSILIVHQRTHTGEKPFECNE CDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCTQ 166 CSMNSHLIWPQKS----HTGEKPYEC--PECGKAFSEKSRLRKHQRTHTGEKPYKC--DG 133 --CGKSFSHMSGLRNHRRTHTGERPYKCDE-CGKAFKLKSGLRKHHRTHTGEKPYKCNQC -CGKTFRQKSNLRGHQRTHTGEKPYECNECGKAFSEKSVLRKH-----105; Conservative 19.2%; Score 386; DB 10; 33.9%; Pred. No. 9.8e-25; 38; Mismatches 125; and Antibodies Length 406; Indels Gaps 222 189 246 17;

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US-09-764-864-909
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SEO ID NO 909
LENGTH: 448
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                      Prior application data removed - consult PALM or NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1045
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CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23
                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                   APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
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               LENGTH: 457
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 19.1%; Score 383.5; DB 10; Length 448; Local Similarity 34.0%; Pred. No. 1.8e-24; ndels 49; es 115; Conservative 40; Mismatches 134; Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 C--NKCGKGFTLKNSLITH-QQTHTG-EKLYTCS--ECGKGFSMKHCLMVHQRTHTGEKP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 CSV--CGKAFSTKFSLTTHQKTHTGEKPYIC--SECGKGFIEKRRLIAHHRTHTGEKPFI 90
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; Sequence 10, Application US/09976165

; Patent No. US20020107383A1
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SEQ ID NO 10
LENGTH: 711
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Best Local Similarity
Watches 93; Conserv
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                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP 69163/1997 PRIOR FILING DATE: 1997-03-05 NUMBER OF SEQ ID NOS: 95
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 08/820,170
PRIOR FILING DATE: 1997-03-19
PRIOR APPLICATION NUMBER: JP 63410/1996
PRIOR FILING DATE: 1996-03-19
PRIOR FILING DATE: 1996-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/976,165
CURRENT FILING DATE: 2001-10-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FUJIWARA, TSUTOMU APPLICANT: WATANABE, TAKESH APPLICANT: HORIE, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/055,699 PRIOR FILING DATE: 1998-04-07
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KPFYCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHT 157
                                        KSYVCI -- ECGQAFIQKAHLIVHQRSHTGEKPYQC -- HNCGKSFISKSQLDIHHRIHTGE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCSLCGKAFSKRSRLTEHQRTHTGEKPYECTE - - CDKAFRWKSQLNAHQKAHTGEKSYIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----QGQGLS----LCQNGESPNCVEDKMLSTVAVLTL 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----KKMKLKVKKSREKRS------LASHLS-----GYIPPKRK-----
                                                                                                                                                                                                                                                                                                                                 PatentIn
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                                                                                                                                 Conservative
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                                                                                                                                                       19.0%; Score 381; DB 1 32.9%; Pred. No. 5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Mismatches 138;
                                                                                                                               43; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 383.5; DB 1
Pred. No. 1.8e-24;
                                                                                                                                                                          DB 10;
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                                                                                                                                                                          Length 711;
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                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Hanzel, David K.

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US-09-864-761-33653, Application US/09864761; Sequence 33653, Application US/09864761; Patent No. US20020048763A1; GENERAL INFORMATION:
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                                                                                                                    RESULT
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LENGTH: 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09828648 Patent No. US20020151510A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/828,648
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/246,331
PRIOR FILING DATE: 2000-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Methods and Compositions for the TITLE OF INVENTION: Treatment of Human Immunodeficie FILE REFERENCE: UNMC 63156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
  APPLICANT:
                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                              666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
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                                                                                                                                                                          TGERPYVCSE--CGKAFNNRSNFNKHQTTHTRDKSYKCSYSVK
                                                                                                                                                                                                    EESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKK-KMKLKVK 313
                                                                                                                                                                                                                                                        ERPFVCYKCGKAFVQKSELITHQRTHMGEK-----PYECLDCGKSFSKKPQLKVH-QRIH
                                                                                                                                                                                                                                                                                               KEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPRE--GCGRTYTTVFNLQSHILSFH 271
                                                                                                                                                                                                                                                                                                                                     GEKPYKCSE--CGKAFTSKSQFKEHQRIHTGEKPYVCTE-CGKAFNGRSNFHKHQITHTR 611
                                                                                                                                                                                                                                                                                                                                                               NEPLFKCTQEGCGKHFASPSKLKRHAKAHEG----YVCQKGCSFVAKTWTELLKH-VRETH 213
                                                                                                                                                                                                                                                                                                                                                                                                                   KPYEC -- SDCGKTFTQKSHLNIH -- QKIHTGERHHVCS -- ECGKAFNQKSILSMHQRIHT
                                                                                                                                                                                                                                                                                                                                                                                                                                           KPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGERPYVCSE--CGKAFNNRSNFNKHQTTHTRDKSYKCSYSVK 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERPFVCYKCGKAFVQKSELITHQRTHMGEK-----PYECLDCGKSFSKKPQLKVH-QRIH
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                   Penn, Sharron G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carlson, Kimberly A.
Gendelman, Howard E.
University of Nebraska Medical Center
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Carlson, Kimberly
Rank, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.0%; Score 381; DB 1 32.9%; Pred. No. 5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119;
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OTHER INFORMATION: MAP TO Z84476.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN BRIATA, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN HELLOW, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
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Best Local
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LENGTH: 525
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234.687
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
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CURRENT FILING DATE: 2001-05-23
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-01-
NUMBER OF SEQ ID NOS: 49117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/236,359 PRIOR FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-08-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
   111
                                                               47
CGKNFSWHSDLILHEQIHSGEKPHVCN--ECGKAFKTRNQLSMHRIIHTGEKPFNC--TQ 166
                                                        CSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGERPFVCAATG 106
                                                                                                                                                     Similarity
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence Listing Engine vers.
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                                                                                                                    Score 379; DB
Pred. No. 5.1e
39; Mismatches
                                                                                                                                               379; DB 10;
No. 5.1e-24;
                                                                                                                       123;
                                                                                                                                                                                Length 525;
                                                                                                                       46;
                                                                                                                       Gaps
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RESULT 8
US-09-864-761-37065
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Sequence 37065, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 948
LENGTH: 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 948, Application US/09764864 Patent No. US20020132753A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prior application data removed - consult PALM or NUMBER OF SEQ ID NOS: 1792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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LOCATION: (335)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                    233 TSVRPYQC-HI-CFKTFVQKQTLKTHMIVHSPVKPFKCKVCGKSFNRMYNLLGHM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                          EESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKK-KMKLKVKKSREKRSLASHL 325
                                                                                                                                                                                                                  QNVRPFVCTECGMEFSQIHHLKQHSLTHKGVKEF~KC--EVCGREFTLQANMKRHML-IH
                                                                                                                                                                                                                                                      THKEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFH
                                                                                                                                                                                                                                                                                        SGRCHYCVE---CGLDFSTLTQLKRHLASHOGPTLYQCLECDKSFHYRSQLQNHMLKH---
                                                                                                                                                                                                                                                                                                                                    NEPLFKCTQEGCGKHFASPSKLKRHAKAHEG -----YVCQKGCSFVAKTWTELLKHVRE 211
                                                                                                                                                                                                                                                                                                                                                                        RPHKCQV--CHKAFTQTSHLKRHM--LLHSEVKPYSCHF--CGRGFAYPSELKAHEVKHE 121
                                                                                                                                                                                                                                                                                                                                                                                                       KPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRWQCRM--CEKSYTSKYNLVTHILGHNGIKPHSCPH--CSKLFKQPSHLQTHLLTHQGT 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCCGKAFQFKHSLTIHGRIHTGEKPYECEE-CGKAFSGSSDLTKHIRIHTGERPYECSKC
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Pred. No. 6.5e-24;
9; Mismatches 125;
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OTHER INFORMATION: EXPRESSED IN BEAIN, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BOAR MARROW, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BT4/4, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BT4/4, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN PLACEMAN, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN PLACEMAN, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3
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PRIOR FILLING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: US 09/632,366
PRIOR FILLING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 624263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILLING DATE: 2000-09-17
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILLING DATE: 2001-01-30
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APPLICANT: Penn, Sharron
                                    Duery Match
Best Local Similarity
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
106;
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Hanzel, David K.
Chen, Wensheng
Conservative
                                    18.5%;
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45;
                                Score 372; DB 10;
Pred. No. 2.1e-23;
Mismatches
                                                                         Length 551;
76;
Gaps
18
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US-09-864-761-37152
; Sequence 37152, Application
; Patent No. US20020048763A1
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                                                                                                                                       PRIOR
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                PRIOR PRIOR PRIOR PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-05-26
                                                                                                       APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
                                                                                                                                       APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2000-10-04
                                                                                    APPLICATION NUMBER: PCT/US01/00670
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                 APPLICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSE-CGKVFLESAALIHHYVIHTGEKPFECLECGKAFNHRSYLKRHQRIHTGEKPFVC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COKGCSFVAKTWTELLKH-VRETHKEEILCEVCRKTFKRKDYLKOHMKTHAPERD-VCRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen, Wensheng
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SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 37152
LENGTH: 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 42958, Application Patent No. US20020048763A1
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                                                                                                                                                                                                                                                                                                   APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                          TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                          PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26
                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                  FILE REFERENCE: Aeomica-X-1
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   PRIOR APPLICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCT 165
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NN: EXPRESSED IN BONE MARROW, SIGNAL = 1.9

NN: EXPRESSED IN HELA, SIGNAL = 2.8

NN: EXPRESSED IN PLACENTA, SIGNAL = 2.8

NN: EXPRESSED IN HEART, SIGNAL = 2.3

NN: EXPRESSED IN BT474, SIGNAL = 2.7

NN: EXPRESSED IN HBL100, SIGNAL = 2.7

NN: EXPRESSED IN HBL100, SIGNAL = 2.6

NN: EXPRESSED IN HBL100, SIGNAL = 0.99

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9

NN: EXPRESSED IN LUNG, SIGNAL = 1.8

NN: EXPRESSED IN LUNG, SIGNAL = 1.8

NN: EXPRESSED IN LUNG, SIGNAL = 1.8

NN: EXPRESSED IN LUNG, SIGNAL = 1.0

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Pred. No. 3.7e-23;
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PRIOR FILING DATE: 2001-01-29
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OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.67

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.59

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.69

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.61

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.61

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.74

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.74

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.61

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.74

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.61

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.74

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.67

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.67

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.74

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.61

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.61

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.61
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                                                                                 180
                            274 SRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21 APPLICATION NUMBER: US 09/508,408 FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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                                                                           KPYECKECGKGFSRVSNLIQHQKTHSSAKPFVCK----ECRKTFRYHYQLTEH-YRIHTG
                                                                                                                           EEILCEVCRKTFKRKDYLKQHMKTHAPERD-VCRCPREGCGRTYTTVFNLQSHILSFHEE 273
                                                                                                                                                                                KPFECKE--CGKAFSLHTQLNHKNIHTGEKPFKC-KECGKSFNRVSNLVQH-QSIHAGV
                                                                                                                                                                                                                                   PLFKCTOEGCGKHFASPSKLKRHAKAHEG --- YVCOKGCSFVAKTWTELLKHVRETHK -- 214
                                                                                                                                                                                                                                                                                        FECKE--CGKFFRRGSNLNQH--RSIHTGKKPFEC--KECGKAFRLHMHLIRHQKFHTGE 123
                                                                                                                                                                                                                                                                                                                                        FVCAATGCDQKFNTKSNLKKHFERKHENOOKQYICSFEDCKKTFKKHQQLKIHQCQHTNE 159
                                                                                                                                                                                                                                                                                                                                                                                          FECK--DCGKAFNRGSNLVQHQSIHTGEKPYEC--KECGKAFRLHLQLSQHEKTHTGEKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 366.5;
Pred. No. 2.6
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RESULT 12
US-09-764-864-1065
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                                                                                                                                SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1065
                                                                                                                                                                                                                                                                       APPLICANT: Rosen et
                                                                                                                                                                                                                                                                                                        Sequence 1065, Application Patent No. US20020132753A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PERL Program
SEQ ID NO 118
LENGTH: 516
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 118, Application US/09974298 Patent No. US20020156263A1
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Best Local
                                                                                                                                                                  Prior application data removed - NUMBER OF SEQ ID NOS: 1792
                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PTZ23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/236,331
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER FILE REFERENCE: PA-0037 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chen, Huei-Mei
                               NAME/KEY: SITE
LOCATION: (289
                                                                             TYPE: PRT
ORGANISM: Homo
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                OTHER INFORMATION:
                                                                  FEATURE:
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 CGKVFSRNSYLVQHLIIHTGEKPYRCNV--CGKVFHHISHLAQHQRIHTGEKPYKC--NE
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                                                                                                                                                                                                                                                                                                                                                                                                                                EHAGCGKTFAMKQSLTRHAVVHDPDK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQS---HILSFHEESRPFVC
                                                                                                                                                                                                                                                                                                                                                                                                              NE--CGKAFSMRSSLTNHHAIHTGEK 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKVFSQNSYLAYHWRIHTGEK-AYKC--NECGK----VFGLNSSLAHHRKIHTGEKPFKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --CGKVFSRNSYLAQHLIIHAGEKPYKCDE-CDKAFSQNSHLVQHHRIHTGEKPYKCDEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGCGKHFASPSKLKRHAKAHEG----YVCQKGCSFVAKTWTELLKHVR-ETHKEEILCEVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCTQ
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SITE
                                 (289)
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Pred. No. 5.5e-23;
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                                                                                                                                                                              Query Match
Best Local Similarity
Matches 116; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 212, Application US/09989920 Patent No. US20020172957A1
                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
SEQ ID NO 212
LENCTH: 610
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes FILE REFERENCE: DEX-0291 CURRENT APPLICATION NUMBER: US/09/989,920 CURRENT FILING DATE: 2001-11-21
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/252,500
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 284
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sun, Yongming APPLICANT: Liu, Chenghua
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 KPFVCAATG------CDQKFNTKSNLKKHFERKHENQQKQY 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 RRFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILMHTGE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 18.3%;
Local Similarity 29.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----CGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKSREKRS-LASH 324
KPFGC--DECGKAFRNNSGLKVHKRIHTGERPYKC--EECGKAYISLSSLINHKSVHPGE 272
                KQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGY 189
                                                           YKCDV--CGKAYISRSSLKNHKGIHLGEKPYKCSY--CEKSENYSSALEQH--KRIHTRE
                                                                                       FVCDYEGGGKAFIRDYHLSRHILTHTGEKPFVCAATGCDQKFNTKSNLKKHFERKHENQQ 129
                                                                                                                      SYNSLLLQHRTIHTGE------RPYVCDV--CGKTFRNNAGLKVHRRLHTGEKP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYECNACGKS----FSRSSHLITHQKIHTGEKPYECNECWRSFGERSDLIKHQRTHTGEK 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KCDE-CGKNFSQNSDLVRHRRAHTGEKPYHCNECGENFSRISHLVQHQRTHTGEK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EC--EECGKSFSRSSHLAQHQRTHTGEKPYECNE--CGRGFSERSDLIKHYRVHTGERPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEG---Y 189
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                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                18.2%; Score 366; DB 9; Length 610; 27.1%; Pred. No. 7.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 366.5; DB 10; Length 547;
; Pred. No. 5.9e-23;
47; Mismatches 116; Indels 81;
                                                                                                                                                                                 52; Mismatches 136;
                                                                                                                                                                                 Indels
                                                                                                                                                                                 124;
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US-09-925-301-1357
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SOFTWARE: PatentIn Ver. 2.
SEQ ID NO 1357
LENGTH: 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1357, Application US/09925301 Patent No. US20020052308A1
                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: PA106
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE LOCATION: (3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                  303
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                                                                                                                                                                                                                                                         46
              HAGCGKTFAMKQSLTRHAVVHDPDK 305
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; NAME/KEY: SITE
LLOCATION: (526)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1357
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
470
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-LECGKAFTHSSSLNNHMRTHSAKK 493
                                                                                                           ECGKAFARSSRLSEHTRTHTGEKPF-ECVK--CGKAFAISSNLSGH-LRIHTGEKPFEC-
                                                                                                                                                                              VCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCE 280
                                                                                                                                                                                                                                          -KICGKSFRNSSCLSDHFRIHTGIKPYKC-KDCGKAFTQNSDLTKHAR-THSGERPYECK
                                                                                                                                                                                                                                                                                                   QEGCGKHFASPSKLKRHAKAHEG---YVCQKGCSFVAKTWTELLKHVRETHKEE--ILCE
                                                                                                                                                                                                                                                                                                                                                                  DCGRAFTVSSCLSQHM--KIHVGEKPYEC--KECGIAFTRSSQLTEHLKTHTAKDPFEC-
                                                                                                                                                                                                                                                                                                                                                                                                                           GCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECGKGFRYSAYLNIHMGTHTGDNPYEC--KECGKAFTRSCQLTQHRKTHTGEKPYKC--K 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DCSANYSKAWKLDAHLCKHTGERPFYCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAAT 105
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Wolffe, Alan
APPLICANT: Wolffe, Alan
APPLICANT: Lal, Albert
APPLICANT: Lal, Albert
APPLICANT: Tan, Siyuan
APPLICANT: Tan, Siyuan
APPLICANT: Gregory, Philip
TITLE OF INVENTION: MODULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
FILE REFERENCE: 8325-0002.21 / S2-US5
CURRENT APPLICATION NUMBER: US/09/942,087A
CURRENT FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/229,037
PRIOR FILING DATE: 1999-01-12
NUMBER OF SEG ID NOS: 43
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 30
LENGTH: 196
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence
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Search completed: February 10, 2003, 17:49:31 Job time: 22 secs
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US-09-942-087A-30
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Best Local Similarity 34.3
Matches 74; Conservative
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                                                                                                           164 -----EKKFACPECPKRFMRSDHLSRHIKTH 189
                                                                                                                                                          204 ELLKHVRETHKEEILCEVCRKTFKRKDYLKOHMKTH 239
                                                                                                                                                                                                                      119 GTTSNLRRHLRWHTGERPFMCTWSYCGKRFTRSSNLQRHKRTHTG----
                                                                                                                                                                                                                                                                     144 KKHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQKGCSFVAKTWT 203
                                                                                                                                                                                                                                                                                                                           62 RTHTGEKKFACPE--CPKRFMRSDELSRHI-KTHQNKKDGGGSGKKKQHICHIQGCGKVY 118
                                                                                                                                                                                                                                                                                                                                                                  92 LTHTGEKPFVCAATGCDOKFNTKSNLKKHFERKHEN------QQKQYICSFEDCKKTF 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                         2 PIPGKKKQHICHIQGCGKVYGQSSDLQRHLRWHTGERPFMCTWSYCGKRFTRSSNLQRHK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.9%; Score 359; DB 9; Length 196;
34.3%; Pred. No. 7.2e-23;
7ative 26; Mismatches 80; Indels 36; Gaps
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Result
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Maximum DB seq
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2: //gn2_6/ptodata/1/paa//pc
3: /cgn2_6/ptodata/1/paa//pc
4: /cgn2_6/ptodata/1/paa//pc
5: //gn2_6/ptodata/1/paa//pc
6: /cgn2_6/ptodata/1/paa//pc
6: /cgn2_6/ptodata/1/paa//pc
8: //gn2_6/ptodata/1/paa//pc
8: //gn2_6/ptodata/1/paa//paa//pc
9: //gn2_6/ptodata/1/paa//paa//pc
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(/cgn2_6/ptodata/1/paa/US086_COMB.pep:*
(/cgn2_6/ptodata/1/paa/US088_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US080_COMB.pep:*
/cgn2_6/ptodata/1/paa/US081_COMB.pep:*
/cgn2_6/ptodata/1/paa/US082_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US084_COMB.pep:*
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first 45 summaries
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   2 US-09-831-426-2

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PCT-US01-18569-2978

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Sequence 2, Appli
Sequence 2, Appli
Sequence 5945, Ap
Sequence 5955, Ap
Sequence 2978, Ap
Sequence 2978, Ap
                                                                                                                          Description
                                                                                                                                                                                           ; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PATENTIN VERS. 2.0
; SEQ ID NO 2
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Human
US-09-831-426-2
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US-09-831-426-2
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GENERAL INFORMATION:
APPLICANT: Hoechst Marion Roussel
APPLICANT: Bordon-Pallier, F.
APPLICANT: Rocher, C.
TITLE OF INVENTION: Human htFIIIA gene and coded htFIIIA protein
FILE REFERENCE: 146.1364
                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/831,426
CURRENT FILING DATE: 2001-05-08
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## ALIGNMENTS

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Ouery Match 100.0%; Score 2008; DB 22; Best Local Similarity 100.0%; Pred. No. 4.8e-164; Matches 365; Conservative 0; Mismatches 0;
61 LCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAATGCDQKFNTKSNLKKH 120
                                                             1 MDPPAVVAESVSSLTIADAFIAAGESSAPTPPRPALPRRFICSFPDCSANYSKAWKLDAH 60
                                                                                                                                                   Indels
                                                                                                                                                                                       Length 365;
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Séquence 2, Application US/09831426C
GEMERAL INFORMATION:
APPLICANT: Hoechst Marion Roussel
APPLICANT: Bordon-Pallier, F.
APPLICANT: Bordon-Pallier, F.
TIPLE OF INVENTION: Human htFIIIA gene and coded hti
FILE REFERENCE: 146.1364
CURRENT APPLICATION NUMBER: US/09/831,426C
CURRENT APPLICATION NUMBER: US/09/831,426C
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Vers. 2.0
SEQ ID NO 2
LENGTH: 365
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; ORGANISM: Human
US-09-831-426C-2
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Matches 365
361 VLTLG 365
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                                                               HDPDKKKMKLKVKKSREKRSLASHLSGYIPPKRKQGQGLSLCQNGESPNCVEDKMLSTVA
                                                                               HDPDKKKMKLKVKKSREKRSLASHLSGYIPPKRKQGQGLSLCQNGESPNCVEDKMLSTVA 360
                                                                                                                        PERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVV
                                                                                                                                       PERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVV 30C
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Pred. No. 4
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CURRENT APPLICATION NUMBER: PCT/US00/26524B
CORRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR PLICATION NUMBER: 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 5945
LENGTH: 409
US-10-106-698-5955, Application US/10106698

Sequence 5955, Application US/10106698

GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION UNMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: SITE LOCATION: (3)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Pred. No. 2.7e-163;
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RESULT 5
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PRIOR FILLING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PATENTIN Ver. 3.0
SEQ ID NO 5955
                                                                                                                                                     SEQ ID NO 2978
LENGTH: 184
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                                                                                                                                                                                                                                                                                                                                          Sequence 2978, Application PC/TUS0118569
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                                                                                                                                                                                 CURRENT APPLICATION NUMBER: PCT/US01/18569
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,467
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                               APPLICANT: Human Genome Sciences, Inc. TITLE OF INVENTION: Nucleic Acids, Proteins FILE REFERENCE: PAl33PCT
NAME/KEY: SITE
LOCATION: (36)
OTHER INFORMATION: :
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                              OTHER INFORMATION:
                                                                           NAME/KEY: SITE
LOCATION: (26)
                                                                                                           FEATURE:
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Pred. No. 2.7e-163;
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RESULT 7
US-09-760-466-1024
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US-10-264-049-2978
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SEQ ID NO 2978
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CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
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TITLE OF INVENTION: Nucleic Acids, Proteins,
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LOCATION: (123)
OTHER INFORMATION: Xaa equals
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OTHER INFORMATION: Xaa equals
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OTHER INFORMATION: Xaa equals any of
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Pred. No. 3.9e-62;
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Pred. No. 3.9e-62;
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US-10-212-083-1024 

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US-09-760-494-255
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US-09-760-466-1024
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                                                                                                                                                                                                                                                                                                            RESULT 9
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LENGTH: 106
TYPE: PRT
ORGANISM: Homo sapiens
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SEQ ID NO 1024
LENGTH: 106
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Best Local
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                                                  TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PTZ59C1N
CURRENT APPLICATION NUMBER: US/10/212,083
CURRENT FILING DATE: 2002-08-06
PRIOR APPLICATION NUMBER: 09/760,466
PRIOR FILING DATE: 2001-01-16
PRIOR EPILICATION NUMBER: 09/179,065
PRIOR APPLICATION NUMBER: 60/179,065
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Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 258
SOFTMARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2001-01-16
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC018
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CURRENT FILING DATE: 2001-01-16
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ59
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APPLICATION NUMBER: 60/180,628
                                    FILING DATE: 2000-01-31
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SEQ ID NO 1024
LENGTH: 106
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GENERAL INFORMATION:
                                                                           SOFTWARE: PatentIn
SEQ ID NO 255
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Best Local :
                                                                                                                                                                                                             PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/223,026
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: 09/760,494
PRIOR FILING DATE: 2001-01-16
PRIOR PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2000-01-31
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TITLE OF INVENTION:
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                                                                                                                      Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/214,886 PRIOR FILING DATE: 2000-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/180,628 PRIOR FILING DATE: 2000-02-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/218,290 PRIOR FILING DATE: 2000-07-14
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PRIOR APPLICATION NUMBER: 60/225,447
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PRIOR APPLICATION NUMBER: 60/217,496
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PRIOR APPLICATION NUMBER: 60/217,496
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         ORGANISM: Homo sapiens
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                                                  LENGTH: 106
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                                                                                                   Ver.
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                                                                                                   2.0
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See File Wrapper or PALM

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Remaining Prior Application data removed - See File Wrapper or PALM
                  260 VFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKSREKR 319
1 VFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKSREKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/214,886 FILING DATE: 2000-06-28
                                                                    27.7%;
illarity 100.0%;
Conservative (
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                                                                                        Score 556; DB 26; 
; Pred. No. 1.3e-39;
                                                                      Mismatches
                                                                                                         Length 106;
                                                                      Indels
                                                                      0
                                                                      Gaps
                                                                      0;
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APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-029

CURRENT APPLICATION NUMBER: PCT/US01/04098A

CURRENT FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: NOV Yet Assigned
PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION UMBER: 09/728,422

PRIOR APPLICATION NUMBER: 09/693,325

PRIOR APPLICATION NUMBER: 09/693,325

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: 09/63,561

PRIOR FILING DATE: 2000-01-5

PRIOR FILING DATE: 2000-09-15

PRIOR FILING DATE: 2000-09-15
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PCT-US01-08631-39706
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APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 21272-049
FULDE REPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILLING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 39706
LENGTH: 95
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Best Local Similarity
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Best Local Similarity
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                       PRIOR
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OTHER INFORMATION: C2H2-TYPE ZINC FINGER SIGNATURE domain identified by eMATRIX,
OTHER INFORMATION: accession number PR00048A, p-value-4.240e-09, raw score of 10.52
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  FILING DATE:
                       APPLICATION NUMBER: 09/654,936
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Pred. No. 1.3e-39;
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Pred. No. 8.6e-31;
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SEQ ID NO 3929
LENGTH: 927
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PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1961, Application PC/TUS0104098A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
                                                                                                  PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/63,561
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: Not Yet Assigned PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: 09/728,422
                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 21272-029
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                                          PRIOR
                                                          PRIOR FILING DATE: 2000-07-19
                                                                                                                                                                                                             PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 09/693,325
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APPLICATION
                     FILING DATE:
                                     APPLICATION NUMBER: 09/598,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 땆
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PY-KCPE--CGKSFSVSSNLINH-QRIHRGERPYIC--ADCGKSFIMSSTLIRHQRIHTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPVVPANEPSLRELVQG-------RPAGAEKPYICN--ECGKSFSQWSKLLRHQ 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVVHDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEKPYECLECGKSFGHSSTLIKHQR-THLREDPFKCPVCGKTFTLSATLLRHQRTHTGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTGEKPYKCPE---CGKRFGQNHNLLKHQKIHAGEKPYRCTECGKSF1QSSELTQHQRTHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQK-GCSFV-----AKTWT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTGEKPYKCTECEKAFTQSTNLIKH-QRSHTG-EKPYKCG--ECRRAFYRSSDLIQHQAT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----AATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVC--------
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                                                                                                                                                                                                                                                                                                                                                                                                             Inc.
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NUMBER: 09/560,875
                     2000-06-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.2%; Score 425; 32.0%; Pred. No. 4
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4.2e-27;
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; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 3960
; SOFTWARE: Custom
; SEQ ID NO 1961
; LENCTH: 869
; TYPE: PRT
ORGANISM: Homo saplens
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                                                               PRIOR APPLICATION NUMBER: Not Yet Assigned PRIOR FILING DATE: 2001-01-30
PRIOR PAPPLICATION NUMBER: 09/728,422
PRIOR PAPPLICATION NUMBER: 09/693,325
PRIOR PAPPLICATION NUMBER: 09/693,325
PRIOR FILING DATE: 2000-10-20
PRIOR PAPPLICATION NUMBER: 09/663,561
PRIOR PAPPLICATION NUMBER: 09/663,561
PRIOR FILING DATE: 2000-09-15
PRIOR PAPPLICATION NUMBER: 09/620,325
PRIOR APPLICATION NUMBER: 09/620,325
PRIOR FILING DATE: 2000-09-01
PRIOR PAPPLICATION NUMBER: 09/598,075
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR PRIOR PAPPLICATION NUMBER: 09/598,075
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR PRILING DATE: 2000-06-20
PRIOR PRILING DATE: 2000-06-20
PRIOR PRILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: PCT/US01/04098A CURRENT FILING DATE: 2001-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides FILE REFERENCE: 21272-029
SOFTWARE: Custom
                                                    NUMBER OF SEQ ID NOS: 3960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401 PY-KCPE--CGKSFSVSSNLINH-QRIHRGERPYIC--ADCGKSFIMSSTLIRHQRIHTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 DVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVVHDP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z1.0%; Score 421; DB 1; Local Similarity 32.0%; Pred. No. 8.6e-27; Pred. No. 8.6e-27; Pred. No. 8.6e-27; Pres. 116; Conservative 41; Mismatches 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 CKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVC------ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 PPAVVAESVSSLTIADAFIAAGESSAPTPPRPA-LPRRFICSFPDCSANYSKAWKLDAHL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DK 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTGEKPYKCPE--CGKRFGQNHNLLKHQKIHAGEKPYRCTECGKSFIQSSELTQHQRTHT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQK-GCSFV-------AKTWT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----AATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIHTGERPNTC--SECGKSFTQSSHLVQHQRTHTGEKPYKCPDCGKCFSWSSNLVQHQRT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 869;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-029-386-32185
                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 32185
LENCTH: 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 32185, Application US/10029386 GENERAL INFORMATION:
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Best Local Similarity
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                   Ouery Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HAZEL, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEDMICA-X-
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 34288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 80
                                                                                                   OTHER INFORMATION: MAP TO Z99130.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 ELLKHVRETHKEEILCEVCRKTFKRKDYLKOHMKTHAPERDVCRCPREGCGRTYTTVFNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 DLLLAEPAEPAPAPAPEEEAEGPAAALGPRGPLGSGPGVVLYLCPEAQCGQTFAKKHQLK 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVVH--DPDKKKMKLKV----KKSRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AHLCKHT---GERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAATGCDQKFNTKS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRSLASHLSGYIPPKRKQGQGL 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGHSIT-HLGTKPFVCPVAGCCARFSARSSLYIHSKKHLQDVDTWKSRCPISSCNKLFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLLRH-----KRK-----HDDDRRF-MCPVEGCGKSFTRAEHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKIHQCQHTNE-PLFKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQ-KGCSFVAKTWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLKAHMKGHEQENSFKCEVCEESFPTQAKLSAHQRSHFEPERPYQCAFSGCKKTFITVSA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLKKHF-------KRHENQQKQYICSFEDCKKTFKKHQQ 148
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47;
                   Score 417.5; DB 24; Length Pred. No. 1.6e-26;
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                                           803;
  93;
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Search completed: February 10, 2003, 17:55:41 Job time: 304 secs
                                                                               410 LFSHNRAHEREQELFSCSFPGCSKQYDKACRLKIHLRSHTGERPFLCDFDGCGWNFTSMS 469
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                                        561 KHSMKTHM----VKRHKVGQDL 578
                                                     318 KRSLASHLSGYIPPKRKQGQGL 339
                                                                                                                                                                            149 LKIHQCQHTNE-PLFKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQ-KGCSFVAKTWT 203
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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4: pir4:*
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Gapop 10.0 , Gapext 0.5
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2008
1 MDPPAVVAESVSSLTIADAF.....ESPNCVEDKMLSTVAVLTLG 365
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

DB ID  Description  2 138937  DNA/RNA-binding pr  Db	Qy 63 Db 61 Qy 123 Db 121 Qy 183 Db 181 Qy 243 Db 241 Qy 303 Db 301 Qy 363 Db 361 RESULT 2 G01496	transcription fact SF RNA-binding pro SF RNA-binding pro zinc-finger protein (cl zinc finger protei finger protein XFO zinc finger protei zinc finger protei finger protein (cl zinc finger protein (cl zinc finger protein (cl selenocysteine tRN finger protein (cl finger protein wire transcription repr transcription repr Krueppel-associate probable finger protei zinc-finger protei zinc-finger protei zinc-finger protei finger protein - A hypothetical prote	TWX1.3 JC1441 JC14495 JC34895 JC34895 JC34895 A34895 A34895 A34896 A54578 B54661 A54661 A54661 A54661 A54661 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B52891 B5289	онавания поповодина на поможнителе на поповодина на поповод	334 348 349 335 339 365 365 626 626 626 626 627 627 627 627 627 627	52.1 52.1 52.1 53.2 54.3 55.1 20.2 27.7 20.2 20.2 20.2 20.2 20.2 20.2	1051.5 1051.5 1047 1047 1025.5 556.5 556.5 543.6 406 406 409 409 398.5 392.5 392.5 392.5 392.5 392.5 392.5 392.5 392.5 392.5 395.5 396.5 396.5 397.5 397.5	. 3 6 5 5 6 5 6 5 6 6 6 6 6 6 6 6 6 6 6 6 6
Score Match Length DB ID Description Qy	Db	DNA/RNA-binding pr	138937	2	363	99.2	1992	1
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362.5	362.5	363	363.5	363.5	364.5	365	365.5	366.5	367	367.5	368	368.5	368.5	371	371
18.1	18.1	18.1	18.1	18.1	18.2	18.2	18.2	18.3	18.3	18.3	18.3	18.4	18.4	18.5	18.5
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A56360	S22954	T12488	138600	JN0533	138598	A37107	S47071	A32891	S51037	A48157	S00833	S35335	A57785	S35305	A48830
zinc finger protei	finger protein zfp	hypothetical prote	zinc finger protei	finger protein pML	zinc finger protei	spermatogenesis pr	finger protein HZF	finger protein 1,	zinc-finger protei	renal transcriptio	finger protein (cl	transcription fact	finger protein ZNF	zinc finger protei	probable transcrip

## ALIGNMENTS

21-Jul-2000 4.E.; Becker, K.G.  30us to Xenopus TFIIIA  piD:g644871  0; Gaps 0;  0; Gaps 0;  111-11-11-11-11-11-11-11-11-11-11-11-1	(man)  puence_revision 29-May-1998 #text_change 4.; Canning, R.D.; Ozato, K.; Biddison, \$  pression analysis of a human cDNA homolog  pression analysis of a human cDNA  pression analy
	RESULT 1 138937 DNA PRA-Phinding profess - buman (fragment)

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transcription factor IIIA - African clawed frog
N:Alternate names: factor A; TFIIIA
C:Species: Xenopus laevis (African clawed frog)
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 21-Jul-2000
C:Accession: A90857; A24961; S21776; A03529; A91007; S40784; S40785
R:Ginsberg, A.M.; King, B.O.; Roeder, R.G.
Cell 39, 479-489, 1984
A:Title: Xenopus 55 gene transcription factor, TFIIIA: characterization of a cDNA clone
A:Reference number: A90857; MUID:85074456; PMID:6210149
A:Accession: A90857
                                                                         A; Molecule type: mRNA
A; Residues: 1-344 <GIN>
A; Cross-references: GB: K02938; NID:g214818;
R; Miller, J; McLachlan, A.D.; Klug, A.
EMBO J. 4, 1609-1614, 1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transcription factor IIIA - human (fragment)
N;Alternate names: TFIIIA
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C;Accession: G01496
A; Contents: annotation R; Smith, J.F.; Hawkins, J.; Leonard,
                                      A:Title: Repetitive zinc-binding domains in A:Reference number: A91007; MUID:85284956; F
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A;Map position: 13q1
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A; Residues: 1-338 <BEC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: GDB:434744; OMIM:600860; Map position: 13q12.3-13q13.1; Superfamily: transcription factor IIIA
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LCCQKGCSFVAKTWTELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAANGCDQKFNTKSNLKKHFE 120
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Pred. No. 3.2
R.E.;
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  Hanas,
                                        PMID:4040853
                                                                                                                  PIDN: AAA49967.1;
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                                                           transcription
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                                                         factor IIIA
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RESULT JC1441

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A.Residues: 1-101 (LIA)

A.Residues: 1-101 (LIA)

R. del Rio, S.; Setzer, D.R.

Nucleic Acids Res. 19, 6197-6203, 1991

A.Title: High yield purification of active transcription factor IIIA expressed in A.Reference number: S40784; MUID:92066468; PMID:1956778

A.Rote: annotation

A.Rote: an engineered sequence was used to obtain high-yield expression in an E. C.Comment: This zinc-containing protein (7-11 Zn/molecule), which interacts with these genes by RNA polymerase III. It also binds the transcribed 5S RNAs.

C.Comment: Most of the Cys and His residues are ligands for zinc binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 40/3; 74/2; 106/3; 136/2; 161/1; 190/1; 266/3; 284/3
C;Superfamily: transcription factor IIIA
C;Keywords: DNA binding; duplication; nucleus; tandem repeat; transcription
F;15-37/Region: zinc finger CCHH motif
F;45-67/Region: zinc finger CCHH motif
F;75-98/Region: zinc finger CCHH motif
F;75-98/Region: zinc finger CCHH motif
F;75-98/Region: zinc finger CCHH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;107-129/Region: zinc finger CCHH motif
F;137-159/Region: zinc finger CCHH motif
F:164-188/Region: zinc finger CCHH motif
F;194-214/Region: zinc finger CCHH motif
F;223-246/Region: zinc finger CCHH motif
F;254-276/Region: zinc finger CCHH motif
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A; Residues: 1-296, 'C', 298-312, 'I', 314-333, 'D', 335-342, 'L', 344 <TSO>
A; Residues: 1-296, 'C', 298-312, 'I', 314-333, 'D', 335-342, 'L', 344 <TSO>
A; Cross-references: EMBL: X036B1; NID: 965111; PIDN: CAB51745-1; PID: 95679716
R; Liao, X.; Clemens, K.R.; Tennant, L.; Wright, P.E.; Gottesfeld, J.M.
J. Mol. Biol. 223, B57-871, 1992
A; Title: Specific interaction of the first three zinc fingers of TFIIIA with
A; Reference number: S21776; MUID: 92167265; PMID: 1538401
A; Accession: S21776
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A:Title: Structure of the gene for Xenopus
A:Reference number: A24961; MUID:86176722;
A:Accession: A24961
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KSKE-KNASVSGTEKTDSLVKNKPSGT
                                                   KRKQGQGLSLCQNGESPNCVEDKMLST
                                                                                                         EEQRPFVCEHAGCGKCFAMKKSLERHSVVHDPEKR--KLKEKCPRPKRSLASRLTGYTPP
                                                                                                                                                               EESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKSREKRSLASHLSGY1PP
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A;Cross-references: GB:M32472; NID:g214150; PIDN:AAA49713.1; PID:g214151
R;Gaskins, C.J.; Hanas, J.S.
Nucleic Acids Res. 18, 2117-2123, 1990
A:Title: Sequence variation in transcription factor IIIA.
A;Reference number: S09653; MUID:90245658; PMID:2110661
A;Accession: S09653
A;Molecule type: mRNA
A;Residues: 1-221,'C',223-234,'E',236-291,'R',293-309,'S',311-313,'A',315-318,'G',320-33
A;Cross-references: EMBL:X17695; NID:g64474; PIDN:CAA35689.1; PID:g64475
C;Superfamily: transcription factor IIIA
C;Keywords: DNA binding; nucleus; transcription factor; zinc finger
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                                                                                                                                                                                                                                                                 transcription factor IIIA - Kenyan clawed frog C:Species: Xenopus borealis (Kenyan clawed frog C:Species: Xenopus borealis (Kenyan clawed frog) C:Date: 20-Jul-1990 #sequence_revision 21-Oct-1992 #text_change C:Accession: B34895; S09653 R:Joho, K.E.; Darby, M.K.; Crawford, E.T.; Brown, D.D. Cell 61, 293-300, 1990 Cell 61, 293-300, 1990 R:Joho K:E.; Barby, M.K.; Crawford, E.T.; Brown, D.D. A:Title: A finger protein structurally similar to TFIIIA that bi A:Reference number: A34895; MUID:90235278; PMID:2331751 A:Accession: B34895 A:Status: preliminary; nucleic acid sequence not shown A:Status: preliminary; nucleic acid sequence not shown
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C:Superfamily: transcription factor IIIA
C:Keywords: DNA binding; duplication; nu
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C;Genetics:
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A; Residues: 1-335 <GAS>
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                                                  ENLRPFVCEHEGCGKTFAMKQSLDRHFNTHDPEKKKM---VKPPRPVRSLASRLSGYKPK
                                                                                     EESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKSREKRSLASHLSGYIP-
                                                                                                                         LH-SEVTCSICNRTFKRKSFLKEHKKIHREERIVYRCPRENCDRTYTTKFNLKSHILTFH
                                                                                                                                                                                               YIHTNQQPFKCSHEGCDKCYASPSRLKRHEKTHAGYPCRKDSTCPFVGKTWSDYMKHAAE
                                                                                                                                                                                                                                CQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQKG--CSFVAKTWTELLKHVRE
             - PKRKQGQGLSLCQNGESPNCVEDKMLSTVAVLTL
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301

244 271 185

211

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transcription factor IIIA - American toad
C:Species: Bufo americanus (American toad)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
C:Accession: JC1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: JCI442
R:Gaskins, C.J.; Smith, J.F.; Ogilvie, M.K.; Hanas,
Gene 120, 197-206, 1992
                                                                                                                                                                                                                                                                        C; Keywords: DNA binding; duplication; nucleus; transcription
                                                                                                                                                                                                                                                                                               A; Gene: TFIIIA C; Superfamily: transcription factor IIIA
                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-339 <GAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Comparison of the sequence and structure of transcription factor IIIA A;Reference number: JC1441; MUID:93013035; PMID:1398134 A;Accession: JC1442
                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X58366; NID:g429028; PIDN:CAA41259.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 184; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 CQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQK--GCSFVAKTWTELLKHVRE
                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THREEILCEVCRRTFKRKDYLKOHMKTHAPERDVCRCPREGCGRTYTTVENLOSHILSFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PALPRREICSEPDCSANYSKAWKLDAHLCKHTGERPEVCDYEGCGKAFIRDYHLSRHILT
HTGEKPCKCETENCNLAFTTASNMRLHFKRAHSSPAQVYVCYFADCGQQFRKHNQLKIHQ
                                          HTGEKPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQ
                                                                                         PVVYKRFICSFPDCNATYNKNRKLQAHLCKHTGERPFPCTYEGCEKGFVTLHHLNRHVLS
                                                                                                                                   PALPRRFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEQRPFACEHAECGKSFAMKKSLERHSVVHDPEKR--KLKEKCPRPKKSLASRLSGCAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EESRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKSREKRSLASHLSGYIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHQEPVMCDECKRTFKHKDYLRNHKKTHKKERTVYRCPRDGCERSYTTAFNLQSHMQSFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTHTQQLPYKCPHEGCDKSFSVPSCLKRHEKVHAGYPCKKDDSCLFVGKTWTLYLKHVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTGEKNFKCDSDKCDLTFTTKANMKKHFNRFHNLQLCVYVCHFEGCDKAFKKHNQLKVHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTGEKPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQ 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVVYKRYICSFADCGASYNKNWKLRAHLCKHTGEKPFPCKEEGCDKGFTSLHHLTRHSIT
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6; Mismatches 80;
                                                                                                                                                                                                      Score 1022; DB 2;
Pred. No. 3.8e-70;
                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                              DB 2;
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RESULT 7

C3.895

C3.895

C; Species: Xenopus laevis (African clawed frog)
C; Species: 20-U1-1990 #sequence_revision 21-Oct-1992 #text_change 21-Aug-1998
C; Accession: C34895
R; Joho, K.E.; Darby, M.K.; Crawford, E.T.; Brown, D.D.
Cell 61, 293-300, 1990
A; Title: A finger protein structurally similar to TFIIIA that binds exclusively
A; Reference number: A34895; MUID:90235278; PMID:2331751
A; Kecession: C34895
A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-365 < JOH>
C; Superfamily: transcription factor IIIA
C; Superfamily: transcription factor IIIA
C; Keywords: DNA binding; zinc finger
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                                   20
                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-365 < JOH>
C; Superfamily: transcri
C; Keywords: DNA binding
                                                                                                                                                                                                                                                                                                            A; Title: A finger protein structurally similar to TFIIIA A; Reference number: A34895; MUID:90235278; PMID:2331751 A; Accession: A34895
                                                                                                                                                                                                                                                                                                                                                                  R;Joho, K.E.; Darby, M.K.; Crawford, cell 61, 293-300, 1990
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
A34895
S RNA-binding protein p43 - Kenyan clawed frog C; Speckes: Xenopus borealis (Kenyan clawed frog C; Date: 20-Jul-190 #sequence_revision 21-Oct-16 C; Accession: A34895
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Best Local
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MKRHLTLKKHSCPTAGCKMTFSTKKSLSRHKLYKH-GDAVPLKCSVPGCKRSFRKKRALR
                                     ILTHTGEKPFYCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLK 150
                                                                           PTEPSKSQVFRCPAAGCKAVYRKEGKLRDHMAGHSEQKLWKCGKKDCGKMFARKRQIQKH
                                                                                                             PPRPALPRRFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSGCTRSFAMRESLLRHLVVHDPERKKLKLKFVRGPSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAGCGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKSREK 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACKKPFKKASALRRHKATHAKKPLQLPCPRQDCDKTFSSVFNLTHHVRNVHLCLQTHRCP 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVCDVPGCSWKSSSVAKLVAHOKRHRGYRCSYEGCQTVSPTWTALQTHVKK-HPLELQCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CPTAGCKMTFSTKKSLSRHKLYKH-GEAVPLKCFVPGCKRSFRKKRALRRHLSVHSNEPL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106;
                                                                                                                                                    108;
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DNA binding; zinc finger
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                                                                                                                                                               27.6%; Score 553.5; DB 2; 37.4%; Pred. No. 1.3e-34;
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                                                                                                                                                    48;
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Pred. No. 7.9e-35;
                                                                                                                                                    Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                        E.T.; Brown,
                                                                                                                                                                                                                                                                                                                                                                                                                           21-Oct-1992 #text_change
                                                                                                                                                                                                                                                                                                not shown
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                                                RESULT 10
S06578
S06578
S06578
C:Species: Xenopus laevis (African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 28-Feb-1990 *sequence_revision 28-Feb-1990 *text_change 3
C:Accession: S06578
C:Accession: S06578
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                       R; Nietfeld, W.; El-Baradi, T.; Mentzel, H.; Pieler, T.; J. Mol. Biol. 208, 639-659, 1989
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       A;Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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   Second-order repeats
                                                                                                                                                                                                          HDQKEKELSSNLVSDVAKK-IINEVTGH
                                                                                                                                                                                                                                             HDPDKKKMKLKVKKSREKRSLASHLSGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity
109; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
       'n
     Xenopus
                                                                                                                                                                                                                                             328
       Laevis
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zinc-finger protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 01-Dec-2000
C;Accession: T37676
R;McDougall, R.C.; Rajandream. M.A.: Rarroll D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Introns: 50/3 C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-374 <MCD>
A;Cross-references: EMBL:AL132675; PIDN:CAB59689.1;
A;Experimental source: strain 972h-; cosmid c144
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: Z21736
A;Accession: T37676
A;Status: preliminary; translated from GB/EMBL/DDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; submitted to the EMBL Data Library, October 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 VHLCLQTHRCPHSNCTRSFAMRESLYRHLVVHDPERKKLKLKFGRRPSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 FICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IHVSEHSNEPLSVCDVPGCGWKSTSAAKLAAHHRRHGGYRCSYEDCQTVSPTWTALQTHL
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                                                                                                                                                                                                                                          LLPYPCTYQDCELRFATKQKLQNHVNRAHEKIISYSCPHESCVGHEGF--EKWSQLQNHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KK-HPLELQCAACKKPFKKASALRRHKATHAKNPLQLPCPRQDCDKIFSTVFNLTHHLRK
                                                     ILSFHEESRPFVCEHAGCGKTFAMKQSLTRH------
                                                                                                                  REAHVPS--CSICGRQFKTAAHLRHHVVLHQTTLEERKTYHCPMEGCKKSFTRSSALKKH
                                                                                                                                                                           RETHKEEILCEVCRKTFKRKDYLKQHMKTH---APERDVCRCPREGCGRTYTTVFNLQSH
                                                                                                                                                                                                                                                                                             EPLFKCTQEGCGKHFASPSKLKRHA-KAHE---GYVC-QKGC----SFVAKTWTELLKHV
                                                                                                                                                                                                                                                                                                                                                         FSCHYDGCDAQFYTQQHLERHIE---VHRKPKPYACTWEGCDECFSKHQQLRSHISACHTH
                                                                                                                                                                                                                                                                                                                                                                                                           FYCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIH-QCQHTN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FHCPYEECGKKYSRPSLLEQHLRTHSNERPFVCDYTGCSKAFYRKSHLKIHKRCHTNVKP
ISVIHEGNMAFHCD--SCGTKFGYKHMLQRHLERGTCKKAHKPYINECGIKHDGIEGVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.7%; Score 496; DB 2; 33.2%; Pred. No. 3.1e-30; tive 48; Mismatches 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSPDB:GN00066;
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proteins Koester, M.; #text\_change 31-Dec-1993

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A; Reference number: S05632; M
A; Accession: S06578
A; Status: not compared with c
A; Molecule type: mRNA
A; Residues: 1-336 <NIE>
C; Keywords: DNA binding; zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                 R:Abrink, M.; Aveskogh, M.; Hellman, L.
DNA Cell Biol. 14, 125-136, 1995
A;Title: Isolation of cDNA clones for 42 different Kruppel-related
A;Reference number: I37566; MUID:95169271; PMID:7865130
A;Accession: I37570
A;Accession: I37570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         zinc finger protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
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A; Residues: 1-693 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: I37570
                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                        Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPFTCTE--CGKNFAQKTNLLCHLKIHTGEKPFTCTECGDKFAKK--NNLLRHLKIHTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FYCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNE 159
KLKV-KKSREKRSLASHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPFTCTECGKAFTLKGSLVGHMKIHTGEKPF-SCTQ--CGKNFTQKNSLLCH-LTMHTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFHEES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLFKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQK-GCSFVAKTWTELLKHVR-ETHK 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSC--TECGKHFAHKGHLVSHM--KTHTGEKPFTCT--ECGKHFAQKGHLVSHMKTHTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FICT -- ECGKGFSQKGILQTHMKTHTGEKPFTC -- TECGKNFAQITTLLRHLTIHTGEKP
                                                                                    QEGCGKHFASPSKLKRHAKAHEG - - - YVCQ - - - KG - - - -
                                                                                                                     -CGKNFRRRSALNNHC--MVHTGEKPYKC--EDCGKCFTCSSNLRIHQRVHTGEKPYKC- 341
                                                                                                                                                      GCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCT 165
                                                                                                                                                                                     ECGKGFSRRSTLTVHCKLHSGEKPYNC--EECGRAFIHASHLQEHQRIHTGEKPFKCDT- 287
                                                                                                                                                                                                                      DCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAAT 105
                                                                                                                                                                                                                                                          105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPFTCTECGKGFALKGNLVLHTKIHTGEKPFSCTQCGKNFAQKNSLLRHLKIHTREKPFT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPFVCEHAG----
                                                 -EECGKCFIQPSQFQAHRRIHTGEKPYVCKVCGKGFIYSSSFQAHQGVHTGEKPYKCNEC
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                                                                                                                                                                                                                                                                     20.2%; Score 406; DB 2; 30.9%; Pred. No. 3.9e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.4%; Score 409; DB 2; 34.0%; Pred. No. 1.1e-23;
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                                                                                                                                                                                                                                                          42; Mismatches
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                                                                                                                                                                                                                                                                                       Length 693
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                                                                                                                                                                                                                                                        74;
                                                                                    -CSFV 198
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138618
              A; Title: Isolation and fine A; Reference number: A57785; A; Accession: I38618
                                                              C; Accession: I38618
R; Tommerup, N.; Vissing,
Genomics 27, 259-264, 19
                                                                                                                 zinc finger protein ZNF143 - human
C:Species: Homo sapiens (man)
C;Date: 23-Feb-1996 #sequence_revision
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A; Residues: 1-542 <FRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A54661; A; Accession: A54661
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A;Status: preliminary
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                                                                                                                                                                                                                                        TECOKAFTDRSNLIKHOKMHSGEKR
                                                                                                                                                                                                                                                                     LKVKKSREKRS-LASHLSGYIPPKR 333
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                                                                 1995
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                                                                                  Ξ.
                             mapping of 16 novel human zinc MUID:96044430; PMID:7557990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 404; DB 2;
Pred. No. 4.3e-23;
                                                                                                                                                                                                                                        537
                                                                                                                 23-Feb-1996 #text_change
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zinc finger protein ZNF41 - human (Iragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 01-Dec-
C;Accession: A54661; I54227
C;Accession: A54661; I54227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GDB:125865; OMIM:314995
A;Map position: Xp11.3-Xp11.23
C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R:Franze, A.; Archidiacono, N.; Rocchi, M.; Marino, M.; Grimaldi, Genomics 9, 728-736, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross - references: GB: M36548; GB: M92443; NID: g340443;
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                                                                                                                                                                                       217 ILCEVCRKTFKRKDYLKQHMKTHAPER-DVCRCPREGCGRTYTTVFNLQSHILSFHEESR 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 CAATGCDOKFNTKSNLKKHFERKHENOOKOYICSFEDCKKTFKKHOOLKIHOCOHTNEPL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 CS--DCGKSFTKKSQLHVHQRIHTGEKPYIC--TECGKVFTHRTNLTTHQKTHTGEKPYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 CSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFV 101
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                                                                                                                        YECSDCGKCFTKKSQLRVHQKIHTGEKDNIC----AECGKAFTDRSNLITH-QKIHTREK
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PYECGDCGKTFTWKSRLNIHQKSHTGERHYECSKCGKAFIQKATLSMHQ1IHTGKKPYAC
                                                                                                                                                                                                                                                       YEC--KDCGKAFIQKSTLSVHQRIHTGEKPYVCPECGKAFIQK--SHFIAHHRIHTGEKP
                                                                                                                                                                                                                                                                                                                   FKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQK-GCSFVAKTWTELLKHVR-ETHKEE
                                                                                                                                                                                                                                                                                                                                                                                      CAE--CGKAFTDQSNLIKH--QKTHTGEKPYKCN--GCGKAFIWKSRLKIHQKSHIGERH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46; Mismatches 121; Indels
                                                            CGKTFAMKQSLTRHAVVHDPDKKKMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           553
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finger-encoding

CUNAS

05-Nov-1999

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A:Cross-references: EMBL:X70680; NID:g453465; PID:g453466 R;Klocke, B.; Koester, M.; Hille, S.; Bouwmeester, T.; Boehm, S.; Biochim, Blophys. Acta 1217, 81-89, 1994 A:Title: The FAR domain defines a new Xenopus laevis zinc finger A:Reference number: S41058; MUID:94114576; PMID:7506934 A:Accession: S65027
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                                                                                                                                                                                                                                                                          A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues; 129-491,'SD',494-581 <NIE> C;Superfamily: zinc finger protein ZFP-36; LIM met C;Keywords: RNA binding; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                          A;Tille: Second-order repeats in Xenopus laevis finger proteins A;Reference number: S05632; MUID:90040698; PMID:2509712 A;Accession: S06544
                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Nietfeld, W.; El-Baradi, T.; Mentzel, H.; Pleler, T.; Koester, J. Mol. Biol. 208, 639-659, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-28; 30-99 < KLW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: S65084
A; Accession: S65088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          finger protein XFO 6 - African clawed frog (fragment) c;Species: Xenopus laevis (African clawed frog) C;Date: 20-Jul-1996 #sequence_revision 27-Feb-1997 #text_change 01-Dec-2000 C;Accession: S6508B; S65027; S06544
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A:Cross-references: GDB:13B991
A:Map position: 11p15.3-11p15.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; RCS 1 duos: 1 + 626 < RES>
A; CCross references: EMBL: U09850;
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, January 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Klocke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Cross-references: EMBL: X70680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: nucleic acid sequence not shown
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                                                                                                                                                                                                            Query Match
Best Local
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311 ECGKSTTEKSILOKH-QRTHTG-EKPFTCT--ECGKSYSAMSTLECHRRTHTGEKPFTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213
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nes 79; Conserv
                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSKPYNCNHCGKTYKQISTLAMHKRT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GERPYYCTEPGCGRAFASATNYKNHVRIHTGEKPYVCTVPGCDKRFTEYSSLYKHHVVHT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRFTCSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEPLFKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQ-KGCSFVAKTWTELLK-HVRET 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPYRCSEDNCTKSFKTSGDLQKHI-RTHTG-ERPFKCPFEGCGRSFTTSNIRKVHVRTHT 340
                                                      GCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCT 165
                                                                                                 ECGKEFTSKYYLNVHKRLHTGEKPFTCTQ--CGKCFSDKSALKYHHKTHTGEKPFAC--T 310
                                                                                                                                              DCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAAT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HKEEILCEVCRKTFKRKDYLKQHMKT 238
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                                                                                                                                                                                            109;
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                                                                                                                                                                                    Score 397.5; DB 2
Pred. No. 1.5e-22;
40; Mismatches 130
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pred. No. 1.3e-22;
30; Mismatches 90;
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                                                                                                                                                                                                                                                                                                LIM metal-binding repeat
                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                            130;
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                                                                                                                                                                                         68;
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-803 <LOV>
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C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
C;Keywords: DNA binding; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GDB:128653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL;X52358;
C;Genetics:
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A; Residues: 476-531 <
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A;Title: Multiple genes encoding zinc finger domains are A;Reference number: 137949; MUID:91145339; PMID:2288909 A;Accession: 137967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Thiesen, H.J
New Biol. 2, 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: A gene encoding 22 highly related A; Reference number: S26823; MUID:91279444; A; Accession: S26823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 *sequence_revision 13-Jan-1995
C;Accession: $26823; 137967; $10416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 19, 2921-2928, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Lovering, R.; Trowsdale, J
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Best Local S
Matches 107
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                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                            CGKAFTQSSNLTTHKKIHTGEK-FYKC--EECGKAFTQSSNLTTH-KKIHTGGKPYKCEE 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E--CGKSFTEKSILRKHHKTHTGEKPFTCTECGKSCTEKSILRKHQITHTGEKPFTCTEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSYSAMSTLKCHRRT-HTGEKPFTCTE--CGKSFTEKSILRKHHKTHTGEKPFTCTECGK
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CGKAFNQFSTLTKHKIIHTEEXPYKCEECGKAFKWSSTLTKHKIIHTGEK---PYKCEEC
                                                                                                                                                                                       QEGCGKHFASPSKLKRHAKAHEG---YVCQKGCSFVAKTWTELLKHVR-ETHKEEILCEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SREKRSLASHLSGYIPPKRKQGQGLSLCQNGESP-----NCVEDK 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKCFSDKTALKYHHKTHTGEKPFACTECGKSFTDKSILRNHQRTHTGEKPF-TCTE--CG
                                                                                                                                                                                                                                           -CGKAFNOFSNLTTH--KRIHTAEKPYKC--EECGKAFSRSSNLTKHKKIHIEKKPYKC-
                                                                                                                                                                                                                                                                                  GCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCT 165
                                                                                                                                                                                                                                                                                                                           ECGKAFKWSSKLTEHKLTHTGEKPYKC -- EECGKAFNWPSTLTKHNRIHTGEKPYKCEV - 452
                                                                                                                   CRKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEH
                                                                                                                                                            -EECGKAFKWSSKLTEHKITHTGEKPYKCEE-CGKAFNHFSILTKHKRIHTGEKPYKCEE
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 394.5; DB 2
Pred. No. 3.4e-22;
4; Mismatches 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from GB/EMBL/DDBC
                                       -CGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKS 315
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PMID:1711675
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  677
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Search completed: February 10, 2003, 17:48:19 Job time : 44 secs	Oy 316 REKRSLAŠHLSGYIPPKRKQGQGLSLCQNGESPNCVEDKMLST 358 :  :     :   :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
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Title:
Perfect score:
Sequence:
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Listing first 45 summaries
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DB seq length: 2000000000
SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
5: sp_invertebrate:*
9: sp_manmal:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:
14: sp_unclassific
15: sp_rvirus:*
16: sp_rvirus:*
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17: sp_archeap:*
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2008
1 MDPPAVVAESVSSIJTI
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                      sp_invertebrate:*
sp_mammal:*
sp_mhc:*
                                                                                                                                      sp_organelle:*
sp_phage:*
                                                                      sp_virus:*
sp_vertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	Bd	ID	Description
_	1583.5	78.9	387	11	Q9CSHB	Q9csh8 mus musculu
2	1582.5	78.8	400	11	Q8VHT7	mus
ω	1498	74.6	336	11	08VHT8	
4.	946.5	47.1	266	11	Q9CSW1	Q9csw1 mus musculu
U	551.5	27.5	368	<u></u>	Q9W7D7	Q9w7d7 oryzias l
6	496	24.7	374	ω	Q9UTL5	Q9utl5 schizosacc
7	425	21.2	927	₽-	Q9UEG4	Q9ueg4 homo sapie
80	416.5	20.7	703	11	Q9R161	Q9r161 mus musculu
9	414	20.6	411	13	P70043	P70043 xenopus 1
10	406.5	20.2	403	G	Q9VXB4	Q9vxb4 drosophila
11	406.5	20.2	559	11	091WM0	Q91wm0 mus musculu
12	406.5	20.2	587	11	Q9Z2X6	Q9z2x6 mus muscu
13	406.5	20.2	700	4	Q961R4	Q96ir4 homo sapien
14	405	20.2	411	<u>1</u> 3	P70046	p70046 xenopus lae
15	405	20.2	847	Α.	Q9Н559	Q9h559 homo sapien
16	404	20.1	531	4	Q9Н176	Q9h176 homo sapien

4.4 5	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26									17
384.5 384.5	385	385.5	385.5	386	386.5	387	389	390.5	390.5	390.5	392	392	392.5	392.5	392.5	393	395	395	396	397.5	397.5	397.5	398	399	399	402.5	403
19.1 19.1	19.2	19.2	•			19.3							19.5						19.	19.	19.	19.	19.	19.	19.	20.	
303 357	600	595	569	578	873	650	744	576	568	346	874	626	715	637	547	751	803	686	436.	720	626	591	891	962	754	756	934
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Q9BY31 Q96JW6	Q91853	Q8TF32	Q96ND8	Q96NH0	Q9XSR1	Q62886	Q62788	Q96N22	Q8TD23	Q62512	Q9R163	070230	Q9UEX4	Q96IR2	Q96QH6	Q9NS43	Q96TE6	Q9NR94	Q96BM3	Q9N003	Q8WUK9	Q09046	061361	061360	Q99J65	061362	Q9VKF1
Q9by31 homo sapien Q96jw6 homo sapien	3 xenc	homo			Q9xsrl canis famil	Q62886 rattus norv	Q62788 rattus norv	nomo	OMO	Q62512 mus musculu	mus	0 mus	homo	homo	homo	homo	homo	homo			Q8wuk9 homo sapien	Q09046 xenopus lae		061360 drosophila	Q99j65 mus musculu	061362 drosophila	09vkf1 drosophila

## ALIGNMENTS

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RESULT
OBVHT7
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8VHT7 PRELIMINARY; PRT; 400 AA. Q8VHT7; Q8VHT7; Q1-MAR-2002 (TrEMBLrel. 20, Created) 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Transcription factor IIIA (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA-binding; Zinc-finger.
NON_TER 1 1
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                                                                    Pfam: PP00096; zf-C2H2; 9.
SMART: SM00355; znF_C2H2; 9.
PROSITE; PS00028; ZINC_FINGER_C2H2_1;
PROSITE; PS50157; ZINC_FINGER_C2H2_2;
                                                                                                                                                                             Gene 282:43-52(2002),

EMBL; AF391799; AAAL69686.1; -.

MGD; MGI:1913846; Gtf3a,

InterPro; IPR000822; Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentia;
NGBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTF3A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE: PS00028; ZINC_FINGER_C2H2_1; PROSITE: PS50157; ZINC_FINGER_C2H2_2;
                                                                                                                                                                                                                                                                                                             Hanas J.S., Hocker J.R., Cheng Y.-G., Lerner M.R., Brackett D.J.,
Lightfoot S.A., Hanas R.J., Madhusudhan K.T., Moreland R.J.;
"CDNA cloning, DNA binding, and evolution of mammalian transcription
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=21673987; PubMed=11814676;
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                                                   NON_TER
                                                                                                                                                                                                                                                                                      factor IIIA.";
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                      400 AA;
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Pred. No. 8.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                      EDFFFA8D8D26EAFD CRC64;
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smatches 47; Indels
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Matches 265
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EMBL; AF391798; AAL59685.1; -.

InterPro; IPR000822; Znf_C2H2.

Pfam; PF00095; Zf-C2H2; 9.

SMART; SM00355; Znf_C2H2; 9.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; UN PROSITE; PS50157; ZINC_FINGER_C2H2_2; 8.
                                                                                                                                                                                                                                        NON_TER
SEQUENCE
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Q8VHT8; Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last seque
Q1-JUN-2002 (TrEMBLrel. 21, Last annot Transcription factor IIIA (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanas J.S., Hocker J.R., Cheng Y.-G., Lerner M.R., Brackett D.J., Lightfoot S.A., Hanas R.J., Madhusudhan K.T., Moreland R.J.; "CDNA cloning, DNA binding, and evolution of mammalian transcription factor IIIA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN; MEDLINE-21673987; PubMed-11814676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                              ALPSRETCSEPDCSASYNKAWKLDAHLCKHTGERSEVCDYEGCGKAPIRDYHLSRHILIH 65
                                                                          ALPRREICSEPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTH
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77.5%;
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23; Mismatches
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Pred. No. 1.1
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RA Arakawa T., Hara A., Fukunishi Y., Konno M., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno M., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Ayons P., Marchionni L., Washima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA Hayashigaki Y., Schoenbach C., Seya T., Kawaji H., Kohtsuki S.,
Query Match
Best Local Similarity
Matches 167; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9CSW1;
Q9CSW1;
01-JUN-2001 (TREMBLRel. 17, Created)
01-JUN-2001 (TREMBLRel. 17, Last sequence update)
01-JUN-2002 (TREMBLRel. 21, Last annotation update)
2610111101R1k protein (Fragment).
GTF3A OR 2610111101R1K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-EMBRYO;
MEDLINE-21085680; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                             Pfam: PF00096; zf-C2H2; 6.

SMART; SM00355; ZnF-C2H2; 6.

PROSITE: PS00028; ZINC_FINGER_C2H2_1;

PROSITE: PS50157; ZINC_FINGER_C2H2_2;
                                                                                                                                                                                                                                                 EMBL; AKOl1845; BAB27876.1; -
HSSP; P03001; 1TF3.
MGD; MGI:1913846; Gtf3a.
Interpro; IPR000082; Znf_C2H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9CSW1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
[1]
                                                                                                                  DNA-binding; Zinc-finger.
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:665-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKSREKRSLASHLSGYIPPKRK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QHTNEPLFRCTHEGCGKHFASPSRLKRHGKVHEGYLCQKGCSFVGKTWTELLKHTREAHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQKGCSFVAKTWTELLKHVRETHK 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEPDCSLPNSTESSSSPEATMLAPAALLTV 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OGOGLSLCQNGESPNCVEDKMLSTVAVLTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEVTCTVCQKMFKRKDHLKQHMKTHAPERDVYRCPREGCARTYTTVFNLQSHILSFHEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFHEES
                                                                                           266
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                           AA;
                                                                                             29048 MW;
                    47.18;
77.78;
  16;
                      Score 946.5;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                           AF2C4738C5B35518 CRC64;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            364
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                      .5e-80
                                             DB 11;
                                           Length
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9
Gaps
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Q9W7D7
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Best Local Similarity
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Q9W7D7;
01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAMM; PFO0096; zf-C2H2; 9.

SMART; SM00195; ZDF_CZBE; 9.

PROSITE; PS00197; ZDEZS_EERREDOXIN; 1.

PROSITE; PS00128; ZINC_FINGER_C2H2_1; 8.

PROSITE; PS00128; ZINC_FINGER_C2H2_1; 6.

PROSITE; PS00157; ZINC_FINGER_C2H2_1; 6.

DNA-binding; Iron-sulfur; Metal-binding; Zinc-finger.

DNA-binding; Iron-sulfur; Metal-binding; Zinc-finger.

SEQUENCE 368 AA; 42356 MW; A0A84CF04C3B144D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MO1. Reprod. --
-!- COFACTOR: BINDS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyldae; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, RNA binding protein 42Sp43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF128814; AAD38911.2; HSSP; P03001; 1TF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ORANGE-RED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryzias latipes (Medaka fish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20070874; PubMed-10602271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-8090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000564; 2Fe2S_ferredoxin.
InterPro; IPR000822; Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Systematic identification of genes
  279
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                                                                                                                                                                                                                                                                                                                                                                                                     FICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKP 99
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CEHAGCGKTFAMKQSLTRHAVVHUPUKKKMKLKVKKSREKRSLASHLSGYIPP
                                                   CGVCEKVYDKAGALRRHKRIHASHKPVLLCPRANCQAYFTTTFNLEHHIRKVHLQLLKYK
                                                                                                   CEVCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFV
                                                                                                                                                         PNFKCSNIRCTATFDSHIARKAHEKKHAGYSCPHKDCQVVEHTWSKLQRHLAK-HPVSFT
                                                                                                                                                                                                         PLFKCTQEGCGKHFASPSKLKRHAKAHEGYVC-QKGCSFVAKTWTELLKHVRETHKEEIL
                                                                                                                                                                                                                                                            FQCKFANCAKSFIDAQRLKKHQNSAHGNH--KFKCNQPKCSLSFKKRRLLKLHLKEHNVH 133
                                                                                                                                                                                                                                                                                                                FVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNE 159
                                                                                                                                                                                                                                                                                                                                                                   FTCTHAGCGACFPREWKLKAHETVHTGERPCACPTAGCGSLFKRTSHLKRHVLQHKGVKG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RKHGNPQKQYVCSYEGCKKAFKKHQQLRTHQCQHTSEPLFRCTHEGCGKHFASPSRLKRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KHTGERPFVCDYEGCGKAFIRDYHLSRHVLIHTGEKPFVCADDGCNQKFNTKSNLKKHIE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAATGCDQKFNTKSNLKKHFE 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 4.96
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 551.5;
Pred. No. 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YB)
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RESULT
Q9UEG4
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Best Local s
Matches 109
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Q9UTL5;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam: PF00096; zf-C2H2; T0.

ProDom: PD000003; znf_C2H2; 1.

SMART; SM00355; ZnF_C2H2; 9.

PROSITE: PS00028; ZINC_FINGER_C2H2_1; 9.

PROSITE: PS00157; ZINC_FINGER_C2H2_2; 9.

DNA-binding; Metal-binding; Zinc-finger.

DNA-binding; Metal-binding; Zinc-finger.

DNA-binding; Metal-binding; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AL132675; CAB59689.1; .
EMBL; AV091590; AAM00046.1; .
HSSP; P07248; lARD.
InterPro; IPR000822; Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McDougall R.C., Rajandream M.A., Churcher C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zinc-finger protein (Transcription SPAC144.09C OR SFC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-972H-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schulman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces
                                                                        315
                                                                                                                                                                                                199
                                                                                                                                                                                                                                                           141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253
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                                                                                                     HDPDKKKMKLKVKKSREKRSLASHLSGY
                                                                                                                                   ISVIHEGNMAFHCD--SCGTKFGYKHMLQRHLERGTCKKAHKPYINECGIKHDGIEGVAI
                                                                                                                                                                ILSFHEESRPFVCEHAGCGKTFAMKQSLTRH-----
                                                                                                                                                                                              REAHVPS -- CSICGROFKTAAHLRHHVVLHQTTLEERKTYHCPMEGCKKSFTRSSALKKH
                                                                                                                                                                                                                            RETHKEEILCEVCRKTFKRKDYLKQHMKTH---APERDVCRCPREGCGRTYTTVFNLQSH 266
                                                                                                                                                                                                                                                         LLPYPCTYQDCELRFATKQKLQNHVNRAHEKIISYSCPHESCVGHEGF--EKWSQLQNHI
                                                                                                                                                                                                                                                                                   EPLFKCTQEGCGKHFASPSKLKRHA-KAHE---GYVC-QKGC----SFVAKTWTELLKHV 209
                                                                                                                                                                                                                                                                                                                   FSCHYDGCDAQFYTQQHLERHIE--VHRKPKPYACTWEGCDECFSKHQQLRSHISACHTH 140
                                                                                                                                                                                                                                                                                                                                                FVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIH-QCQHIN 158
                                                                                                                                                                                                                                                                                                                                                                               FHCPYEECGKKYSRPSLLEQHLRTHSNERPFYCDYTGCSKAFYRKSHLKIHKRCHTNVKP
                                                                                                                                                                                                                                                                                                                                                                                                           FICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                           al Similarity
109; Conserv
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(TrembLrel. 13, Last sequence update)
(TrembLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                         24.7%; Score 496; DB 3 33.2%; Pred. No. 7e-38; tive 48; Mismatches 1
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Best Local
         Q9R161;
Q9R161;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagase T., Ishikawa K., Nakajima D., Ohira M., Seki N., Miyajima N. Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. V. The complete sequences of 100 new cDNA clones from brain which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9UEG4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00096; zf-C2H2; 19. PRINTS; PR00048; ZINCFINGER. SMART; SM00355; ZnF_C2H2; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB002324; BAA20784.1; HSSP; P08047; 1SP2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-binding; Metal-binding; Nuclear protein; Zinc-finger NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00028; ZINC_FINGER_C2H2_1; 19.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Res. 4:141-150(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97349984; PubMed-9205841;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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116; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPAVVAESVSSLTIADAFIAAGESSAPTPPRPA-LPRRFICSFPDCSANYSKAWKLDAHL
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                                                                                                                                                                                                                                                                                                                   HTGEKPYKCPE - - CGKREGQNHNLLKHQKIHAGEKPYRCTECGKSFIQSSELTQHQRTHT
                                                                                                                                                                                                                                                                                                                                                                                                                                         RIHTGERPNTC--SECGKSFTQSSHLVQHQRTHTGEKPYKCPDCGKCFSWSSNLVQHQRT
                                                                                                                                                                                                                                                        GEKPYECLECGKSFGHSSTLIKHQR-THLREDPFKCPVCGKTFTLSATLLRHQRTHTGER
                                                                                                                                                                                                                                                                                                                                                HTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQK-GCSFV-----AKTWT
                                                                                                                                                                                                                                                                                                                                                                               HTGEKPYKCTECEKAFTQSTNLIKH-QRSHTG-EKPYKCG--ECRRAFYRSSDLIQHQAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPVVPANEPSLRELVQG------RPAGAEKPYICN--ECGKSFSQWSKLLRHQ 227
                                                                                                                                                                305
                                                                                                                                   514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            large proteins in vitro.";
4:141-150(1997).
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0096; zf-C2H2; 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         927 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          -AATGCDOKENTKSNLKKHEERKHENOOKOYICSFEDCKKTEKKHOOLKIHOCO 155
         (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                       PRELIMINARY;
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                                                                                                                                                                                              -CGKSFSVSSNLINH-QRIHRGERPYIC--ADCGKSFIMSSTLIRHQRIHTG
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Primates;
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20,
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         Created)
Last sequence update)
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Pred. No. 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176C78A9C407F8C0 CRC64;
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.6e-31;
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Best Local Sim
Matches 115;
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PROSITE; PS50805; KRAB; 1.

PROSITE; PS500528; ZINC_FINGER_C2H2_1; 15.

PROSITE; PS50157, ZINC_FINGER_C2H2_2; 15.

DNA-binding; Metal-binding; Nuclear protein; Zinc-fing DNA-binding; Metal-binding; Nuclear protein; Zinc-fing SEQUENCE 703 AA; 79398 MW; 1AlDA000D10D7386 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00349; KRAB; 1.
SMART; SM00355; ZnF_C2H2; 15.
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                                                                                                                                     P70043;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Hauser L., York M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                             Xenopus laevis (African clawed frog)
                                                                                                                         Zinc
                                                                                                                                                                                                                                  P70043
                                                                                                                                                                                                                                                                                                                                             595
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                                                                                                                  finger protein XFDL 141
                                                                                                                                                                                                                                                                                                                                             DTCGKAFSQRSNLQVHQIIHTGEKPFKCEECGKEFSWSAGLT 636
                                                                                                                                                                                                                                                                                                                                                                                                                                   E--CGKGFSQASNLQAHQSVHTGEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DE--CGKRFSLSFNLHSHQRVHTGEKPYKCEE-CGKGFSSASSFQSHQRVHTGEKPFCCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TQEGCGKHFASPSKLKRHAKAHEG - - - YVCQKGCSFVAKTWTELLKHVR - ETHKEEILCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --CGKGFTQRSHLQAH-ERIHTG-EKPYKCG--DCGKRFSCSSNLHTHQRVHTEEKPYKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCDOKFNTKSNLKKHFERKHENOQKQYICSFEDCKKTFKKHQOLKIHQCQHTNEPLFKC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PECGKSFNQSSHLYAHLPIHTGEKPYCCD--NCGKGFSRSTDLNIHCRVHTGEKPYKCEV 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAA 104
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                                                                                                                                                                                                                                                                                                                                                                                      -----RKQGQGLSLCQNGESP-NCVE-DKMLSTVAVLT 363
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                                                                                                                                                                                                                                  PRELIMINARY;
                                 Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 416.5;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomı;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ---PFKCNACQKRFSQASHLQAHQRVHTGERPYKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .4e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SGYIPPK- 332
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         RESULT
Q9VXB4
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li p.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Adbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Chenry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9VXB4 PRELIMINARY;
Q9VXB4;
Q1-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00096; zf·C2H2; 12.
PRINTS; PR00048; ZINCFINGER:
ProDom; PD000003; Znf_C2H2; 3.
SMART; SM00355; ZnF_C2H2; 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CG9609 protein CG9609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00028; ZINC_FINGER_C2H2_1; 12.
PROSITE; PS50157; ZINC_FINGER_C2H2_1; 12.
DNA-binding; Metal-binding; Nuclear protein;
SEQUENCE 411 AA; 46615 MW; 0F3984747406A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U65897; AAB07010.1; HSSP; P25490; 1UBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "XFDL 141."
                                                                                                                                                                                                                                                                        MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECGEQF - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QKGCSFVAKTWTELLKHVRETHKEE--ILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTECGKSFAAKKNLKRHOMIHTGEKPHECTE--CGKQFLEKSKLKRHHLSHTGVKPFSCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---CKKTFKKHQQLKTHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEG---YVC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VC--TECGKSFRKKCELKSHLQ--VHTGVKQFVCTECGKSFRDRSELNIHINVHTGKTFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VCAATGCDQKFNTKSNLKKHFERKHENQQKQYIC----SFED-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VC--PHCGKSYRDKTKLTVHLRIHTGETPFVC--PECGKGFRDASFLKSHLSIHTGEKPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LD35155P).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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DB 13; .2e-30;

Length Indels

Zinc-finger.

107;

50;

Gaps

15;

191

294

249

138 180

403

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Brachycera; Muscomorpha;

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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Allali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., Mopherson D.,
RA Mcrkulov G., Milshina N.V., Mobarry C., Mcreis J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pecleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pecleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Wen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q. Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng Y.,
RA Gibbs R.A., Weers E.W., Rubin G.M., Venter J.C.,
RT The genome sequence of Drosophila melanogaster.",
RN Colence 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Sim
Matches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., A Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R A Gonzalez M., Guerin H., Li P., Liao G., Miranda A., Mungali C.J Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan Yu C., Lewis S.E., Rubin G.M., Celniker S.;

L Submitted (Auf-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AE003503; AAF48663.1; -.

R EMBL; AF051849; AAK93273.1; -.

R HSSP; P03001; 1TF6
R Flyase; FB9003787; CG9609.

R Interpro; IPR00822; Znf C2H2.

R Flyase; FB900355; Znf-C2H2; 8.

R PROSITE; PS00157; ZNC_FINGER_C2H2_1; 8.

PROSITE; PS00157; ZNC_FINGER_C2H2_2; 7.

DNA-binding; Metal-binding; Zinc-finger.

DNA-binding; Metal-binding; Zinc-finger.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BERKELEY;
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318 KRSLASHLSGYIPPKRKQGQGLSLCQNGESPNCVEDKMLSTVAVLTL
                                                                                                                                                 259
                                                                                                                                                                                                                          208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
                                                                 YLRNLRQHMLTAH-SGRRFECQALDCGRCFSSAQNLARHLLRDHKDGATKKELKAKKKDK
                                                                                                                                                 TVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAV-VHDPDKKKMKLKVKKSRE
                                                                                                                                                                                                                          SLHGKNRHK---
                                                                                                                                                                                                                                                                                        T----HKEEILCEVCRKTFKRKDYLKQHMKT---HAPERDVC----RCPREGCGRTYT
                                                                                                                                                                                                                                                                                                                                                                 EIREHTLEYPYSCSK--CSRCFYQQWQCQSHEPSCKLYEC-PGCPLQFDKWTLYTKHCRD
                                                                                                                                                                                                                                                                                                                                                                                                                                  QC-QHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQKGCSFVAKTWTELLKHVRE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESAAKKTVKCALEECSKMFISVSNMTRHMRETHES-PKVYPCS--QCSAKFSQKLKLKRH 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --TGEKPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIH 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYACSMPKCEATFKRLDQLDRHEYHHTGIKKHACSYEGCDKTYSIVTHLKRHLRSTHERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RFICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHI-LTH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Pred. No. 1.5e-29;
5; Mismatches 144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              George R.,
ngall C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S., Wan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
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                                                                                                                                                                                                                                                                                            258
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RESULT
OPERATOR
                                                                                                                                                                                                           RESULT 12
Q9Z2X6
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Best Local S
Matches 98
                                                                                                                                 Q922X6;
01-MAY-1999
01-MAY-1999
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001
01-DEC-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q91WM0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01352; KRAB; 1.
Pfam; PF001352; KRAB; 1.
Probom; PF000003; Znf_C2H2; 6.
PROSITE; PS50805; KRAB; 1.
PROSITE; PS50028; ZINC_FINCER_C2H2_1; UNKNOWN_14
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 15.
DNA-binding; Hypothetical protein; Zinc-finger.
SEQUENCE 559 AA; 64216 MW; C08F544C0EZA429C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
STRAIN-C57B6;
              SEQUENCE FROM
                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                             Q9Z2X6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL: BC014712: AAH14712.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-EYE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical 64.2 kDa protein.
                                          NCBI_TaxID=10090;
                                                                                       Mus musculus (Mouse)
                                                                                                                    Zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001909; KRAB.
InterPro; IPR000822; Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                    275
                                                                                                                                                                                                                                                                                                                               446
                                                                                                                                                                                                                                                                                                                                                              216
                                                                                                                                                                                                                                                                                                                                                                                           389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323
                                                                                                                                                                                                                                                                       501 KPYVCKQ--CGKAFTLSSSLRRHDVVHSEEK 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YVCK--HCGKAYTTYNTLRAHERSHTGEKPYVCKH--CGKAYTSYSTLRAHERSHTGEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKTGEGGKTKSTSRKRRRDAGRS-----KHSRLSKLACLQL 358
                                                                                                                                                                                                                                                                                                  RPFVCEHAGCGKTFAMKQSLTRHAVVHDPDK 305
                                                                                                                                                                                                                                                                                                                               PYSCKLCGKAFTHSNYLQIHKRIHTGEKPYVCK----ECGKAFARSTSLHIH-EGTHSGE
                                                                                                                                                                                                                                                                                                                                                            EILCEVCRKTFKRKDYLKQHMKTHAPERD-VCRCPREGCGRTYTTVFNLQSHILSFHEES
                                                                                                                                                                                                                                                                                                                                                                                           KPYVCKQ--CGKAFAQSSYLHIHQRSHTGEKPYVCKQCGKAFTRSSHLQIHK-ITHTGEK
                                                                                                                                                                                                                                                                                                                                                                                                                       PLFKCTQEGCGKHFASPSKLKRHAKAHEG---YVC-QKGCSFVAKTWTELLKHVRETHKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     YVC--KHCGKAFTQSSYLRIH-KRTHTG-EKPYIC--KQCGKAFARSSHLQIHKRSHTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                  9 (TrEMBLrel. 10,
9 (TrEMBLrel. 10,
2 (TrEMBLrel. 21,
r protein sll-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
TISSUE-SPLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RETINA;
                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update
                                                                                                                                  Last sequence update)
Last annotation update
                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 406.5; DB 11; Length Pred. No. 2.2e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                          Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ein; Zinc-finger.
C08F544C0E2A429C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                              587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                          445
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RESULT 13
Q961R4
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        S KWERRER BRANCH DE TRANSPORTE DE L'ARCHE DE
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                                                        A Strausberg R.;

Submilted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL, BC007303, AAH07303.1; -.

R InterPro; IPR001909; KRAB.

R InterPro; IPR00082; Znf_C2H2.

R Pfam; PF01352; KRAB; 1.

R Pfam; PF00096; Zf-C2H2; 19.

R Pfam; PF000095; Znf_C2H2; 5.

R Pf0D0m; PD000003; Znf_C2H2; 19.

R PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_18.

RPROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_18.

RPROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_18.

RPROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001909; KRAB.
InterPro; IPR000822; znf_C2H2.
InterPro; IPR000822; znf_C2H2.

R Pfam; PF01152; KRAB, 1.

R PF1NTS; PR00048; ZINCFINGER.
R PR1NTS; PR000035; znf_C2H2; 15.
R PR1NTS; SN00349; KRAB, 1.
R SMART; SN00349; KRAB, 1.
R SMART; SN00355; znf_C2H2; 15.
R SMART; SN00355; znf_C2H2; 15.
R SMART; SN00355; znf_C2H2; 15.
R SMOSITE; PS00028; ZINC_FINGER_C2H2_1; 15.
R PROSITE; PS00028; ZINC_FINGER_C2H2_2; 16.
R PROSITE; PS00028; ZINC_FINGER_C2H2_1; 15.
R PROSITE; PS00028; ZINC_FINGER_C2H2_1; 15.
R PROSITE; PS00028; ZINC_FINGER_C2H2_1; 16.
R PROSITE; PS00028; ZINC_FINGER_C2H2_1; 15.
R PROSITE; PS00028; ZINC_FINGER_C2H2_1; 15.
R PROSITE; PS00028; ZINC_FINGER_C2H2_1; 16.
R PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O-Wang J.;
"Zinc finger protein.";
"Zinc finger protein.";
"Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AB020542; BAA34724.1; -.
HSSP; P08047; 1SP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to zinc finger protein 224.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q961R4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q961R4
                                    DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-EYE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYSCKLCGKAFTHSNYLQIHKRIHTGEKPYVCK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLFKCTQEGCGKHFASPSKLKRHAKAHEG----YVC-QKGCSFVAKTWTELLKHVRETHKE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FVCAATGCDOKFNTKSNLKKHFERKHENOOKQYICSFEDCKKTFKKHQQLKIHQCQHTNE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YVCK--HCGKAYTTYNTLRAHERSHTGEKPYVCKH--CGKAYTSYSTLRAHERSHTGEKP 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FICSFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPYVCKQ--CGKAFTLSSSLRRHDVVHSEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPEVCEHAGCGKTFAMKQSLTRHAVVHDPDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YVC--KHCGKAFTQSSYLRIH-KRTHTG-EKPYIC--KQCGKAFARSSHLQIHKRSHTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EILCEVCRKTFKRKDYLKQHMKTHAPERD-VCRCPREGCGRTYTTVFNLQSHILSFHEES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPYVCKQ--CGKAFAQSSYLHIHQRSHTGEKPYVCKQCGKAFTRSSHLQIHK-ITHTGEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
700 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
    80559 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.2%;
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
    79F266EA18821193 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; DB 11;
2.4e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
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RESULT
P70046
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Best Local Similarity
Matches 120; Conserv
  Matches
                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P70046;
P70046;
01-FEB-1997
01-FEB-1997
                                                                                     Pfam; PF00096; zf-C2H2; T2.
PRINTS; PR00048; ZINCFINGER.
ProDoom; PD000003; Znf_C2H2; 3.
SMART; SM00355; ZnF_C2H2; 12.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 12.
PROSITE; PS0157; ZINC_FINGER_C2H2_2; 12.
DN-binding; Metal_binding; Nuclear protein; Zinc DN-binding; Nuclear Protein; 
                                                                                                                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: EMBL; U67077; AAB72012.1; HSSP; P25490; 1UBD.
                                                                                                                                                                                                                                                                                                                                                                                               gene encoding two structurally 
Xenopus laevis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=97321550; PubMed=9178260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFDLAMA.

Xenopus laevis (African clawed frog).

Xenopus laevis (African clawed frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XFDL141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1997 (TrEMBLrel.
01-FEB-1997 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bellefroid E., Bourguignon C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-8355
                                                                                                                                                                                                                                                                                InterPro; IPR000822; Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                                                           Mech.
                                                                                                                                                                                                                                                                                                                                                                                                                      "Transcription regulation and alternative splicing gene encoding two structurally distinct zinc finge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pieler T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopodinae;
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                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKSFRMKIHYQVHLVVHTGEKPYKCEVCGKAFRQSSYLKIHLKAHSVQKPF-KC--EECG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKTWTELLKH----VRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QEGCGKHFASPSKLKRHAKAHEG --- YVCQ --- KG --- -- --- --- --- --- --- CSFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECGKGFSRRSTLTVHCKLHSGEKPYNC--EECGRAFIHASHLQEHQRIHTGEKPFKCDT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPFVCAAT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQASHLLTHQRVHSGEK - - - PFKCEECGKSFSRSAHLQAHQKVHTGEKPYKCGECGKGFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMKQSLTRHAVVHDPDKKKMKLKVKKSREKRSLASHL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTYTTVFNLQSHILSFHEESRPFVCEHAG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -CGKNFRRRSALNNHC--MVHTGEKPYKC--EDCGKCFTCSSNLRIHQRVHTGEKPYKC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -EECGKCFIQPSQFQAHRRIHTGEKPYVCKVCGKGFIYSSSFQAHQGVHTGEKPYKCNEC
  104;
                                                                                                                                                                                                                                                                                                                                                                           Dev. 63:99-108(1997).
                      Similarity
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  Conservative
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                      35.6%;
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21,
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  31;
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Pred. No. 2.9e-29;
                    Score 405;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bouwmeester T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411
                           N
                      2e-29;
                                             DB 13;
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  107;
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                                                                                          Zinc-finger
704 CRC64;
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                                          Length 411;
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  50;
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RESULP

OPHS559

AC OPH

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09H559 PRELIMINARY; PRI; 647 Am.
09H559;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
BA526DB.4 (Novel KRAB box containing C2H2 type zinc finger protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01352; KRAB; 1.

Pfam; PF00096; zf-C2H2; 17.

PRINTS; PR00040; ZINCFINGER.

SMART; SM00349; KRAB; 1.

SMART; SM00355; ZNF_C2H2; 17.

PROSITE; PS00085; KRAB; 1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 14.

PROSITE; PS00028; ZINC_FINGER_C2H2_2; 18.

DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.

NON TEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
EMBL; AL135981; CAC1728.1; -.
HSSP; P07248; 1paa.
InterPro; IPR001909; KRAB.
InterPro; IPR001909; KRAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                    YECSE - - CGKAFIQKSTLSMHQRIHRGEKPYVCTECGKAFFHK - - SHFITHERIHTGEKP
                                                                                                                   FKCTQEGCGKHFASPSKLKRHAKAHEG---YVCQK-GCSFVAKTWTELLKHVR-ETHKEE 216
                                                                                                                                                                                     C--TVCGKAFTDRSNLIKH--QKIHTGEKPYKCS--DCGKSFTWKSRLRIHQKCHTGERH 546
                                                                                                                                                                                                                    CAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLKIHQCQHTNEFL 161
                                                                                                                                                                                                                                                                                                     CS--DCGKSFIKKSQLHVHQRIHTGENPFIC--SECGKVFTHKTNLIIHQKIHTGERPYI 492
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                                                           FVCEHAG-----
                                                          -CGKTFAMKQSLTRHAVVHDPDKKKM--
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Search completed: February 10, 2003, 17:47:29 Job time: 89 secs

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## ALIGNMENTS

AAA15405 ID AAA1

AAA15405 standard;

DNA; 1273

ВP

04-SEP-2000

(first entry)

AAA15405;

RESULT 1

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CDS
Bordon-Pallier F,
                    10-NOV-1998;
                              09-NOV-1999;
                                       18-MAY-2000.
                                                 WO200028024 - A1
                                                                                     Homo sapiens.
                                                                                               cancer;
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                                                                                               SS
                    98FR-0014146.
                              99WO-FR02738
                                                          /product=
                                                                      Location/Qualifiers 176..1273
                                                                /*tag=
Rocher C;
                                                          "transcription factor"
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Human; transcription factor; htfIIIA; DNA-binding protein; transcription; ribosomal RNA 5S gene; transcriptional control;

DNA encoding a human transcription factor designated htfIIIA.

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Best Local Similarity
Matches 1273; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes a human transcription factor designated htfIIIA. The polypeptide is probably a DNA-binding protein probably involved in initiating transcription of the gene for ribosomal RNA 5s and maintaining the stability of transcription of other control genes and maintaining the stability of transcription of other control genes the htfIIIA polynucleotides and polypeptides are used to make therapeutic or diagnostic compositions for diseases associated with disorders of transcriptional control, particularly cancer or other inherited diseases. The htfIIIA polynucleotide can also be used to detect anomalies in gene transcription, particularly for diagnosis of
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CAAGTGTACCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACA
                                    CAAGTGTACCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACA
                                                                                                CTTTAAGAAACATCAGCAGCTGAAAATCCATCAGTGCCAGCATACCAATGAACCTCTATT
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DB; AAY93317.
                                                                           CTTTAAGAAACATCAGCAGCTGAAAATCCATCAGTGCCAGCATACCAATGAACCTCTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease, also for studying diseases involving hTFIIIA.
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nilarity 100.0%;
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Human: ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; radult resperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease;
                                        03-OCT-2000;
                                                                                   03-OCT-2001;
                                                                                                                                                                                                                                                  granulocyte activation; chronic inflammation; allergy
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CGCAD, by detecting the level of expression of gene(s) (GS) identified by CC DNA chip analysis as given in the specification, and comparing CC the expression level to an expression of gene(s) (GS) identified by CC Also included are modulating (M2) GA by contacting GC with an agent CC GC, where differential expression of Gs is indicative of GCA.

CC Also included are modulating (M2) GA by contacting GC with an agent CC chronic) in a tissue, an altergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease using the CC chronic) in a tissue, an altergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease, by detecting the Level of expression in a sample of the tissue of gene(s) from Gs, where CC the level of expression of the gene is indicative of inflammation; where CC an altergic response in a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, or an altergic response in a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, or inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for screening an agent capable of modulating GA; M3 is useful for screening an agent capable of modulating GCA; M2 is useful for cresponse in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease, and affection, protozoal infection, fundal infection, protozoal infection, protozoal infection, protozoal infection, protozoal infection, protozoal infection, strail infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1381
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                                                                               TCCGCCGGCCGTGGTCGCCGAGTCGGTCGTCCTTGACCATCGCCGACGCGTTCATTGC
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                                                                                                                                          Internal control region of the 55 gene. The coding region (Claimed) is given in AAT14037. A fragment lacking a 5'-portion of the gene has been isolated from a human foetal brain cDNA library (OTK7-1), and the 5'-portion of the gene has been isolated by 5'-rapid amplification of cDNA ends using primers H11-R (AAT14039), H11-E (AAT14040), H11-E (AAT14040), H11-E (AAT14041) and Ap-2 (AAT14042), complementary anchor primer AAT14043. Reverse transcription using H-11R is followed by anchor primer ligation and ECR using Ap-2 and H11-E, to give a full-length cDNA, OTK7. The gene and its encoded protein may be used in diagnosis, identification or therapy of hereditary diseases such as cancer, or other diseases resulting from abnormal transcriptional control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer; PCR; polymerase chain reaction; foetal brain;
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      The sequence encodes human transcription factor-IIIA (hTFIIIA), a DNA binding protein with 9 zinc finger domains, which is necessary for the initiation of 5s RNA gene transcription, binding to an internal control region of the 5s gene. A fuller cDNA sequence with flanking regions is given in AAT1403B. A fragment lacking a 5'-portion of the gene has been isolated from a human foetal brain cDNA library (OTK7-1), and the 5'-portion of the gene has been isolated by 5'-rapid amplification of cDNA ends using primers H11-R (AAT14039), H11-E (AAR14040), H11-H (AAR140401) and AP-2 (AAT14039), H1-E (AAR14040), H11-H (AAR140401) and PCR using AP-2 and H11-E, to give a full-length cDNA, OTK7. The gene and its encoded brotein may be used in diagnosis, identification or therapy of hereafters, discountered from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; transcription factor-IIIA; hTFIIIA; DNA binding protein; ribosome; zinc finger; rapid amplification of cDNA ends; 5'-RACE; primer; PCR; polymerase chain reaction; foetal brain; anchor primer; diagnostic; probe; transcription control; antitumour; cancer; therapy; ss.
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                 The present sequence represents a fragment of a human transcription factor (designated htfIIA) gene. The polypeptide is probabaly a DNA-bhoding protein probably involved in initiating transcription of the gene for ribosomal RNA 5S and maintaining the stability of transcription of other control genes. The htfIIIA polynucleotides and polypeptides are used to make therapeutic or diagnostic compositions for diseases associated with disorders of transcriptional control, particularly cancer or other inherited diseases. The htfIIIA polynucleotide can also be used to detect anomalies in gene transcription, particularly for diagnosis of inherited disease, also for studying diseases involving hTFIIIA.
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                                                                                                                                                                 Claim
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                                                                                                                                                 cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing
                                                                                                                                                                                                                                                                                                                            Nucleic
useful f
            present invention.

N.B. Pages 666 to 682 and page 7053 of the missing at time of publication, meaning no SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54313-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antiqens, and the use of ovarian antiqens polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and
                                                                                                                                                                                                                             Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndro PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; energy disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cystatic; inmunomodulatory; neuroprotective; antibody preparation; cystatic; reproductive; chromosome 13g12.3-13
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                                                                                                                                                                         TTGGCCTCTCATCTCAGTGGATATATCCCCTCCAAAAGGAAACAAGGGCAAGGCTTATCT
                                                                                                                                                                                                                                                                                                                             CATGCTGGCTGTGGCAAAACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTA
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Note: With the exception of SEQ ID No 1 and 2, for this patent did not form part of the prints
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to polynucleotides encoding colon tumour proteins. The polynucleotides and encoded polypeptides are useful in pharmaceutical compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polynucleotide sequences may be used as hybridisation probes or primers, and in the design and preparation of the primers of the diagnosis of the design and preparation of the design and the design an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-2000; 2000US-223283P
28-MAR-2001; 2001US-279763P
29-JUN-2001; 2001US-302051P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating at immune response against cancer, particularly for the immunotherapy of colon cancer, and as markers for the progression of cancer.

ABK44450-ABK46237 represent coding sequences of human colon tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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AAAATGAAGCTCAAAGTCAAAAAATCTCGTGAAAAACGGAGTTTGGCCTCTCATCTCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tent did not form part of the printed specification but was the European Patent Office.
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                                                                                                                                                                                                            Query Match
                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                    for this supplied
                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to polynucleotides encoding colon tumour proteins. The polynucleotides and encoded polypeptides are useful in pharmaceutical compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polynucleotide sequences may be used as hybridisation probes or primers, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating an immune response against cancer, particularly for the immunotherapy of colon cancer, and as markers for the progression of cancer.

ABK44450-ABK46337 represent coding sequences of human colon tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-2000; 2000US-223283P
28-MAR-2001; 2001US-279763P
29-JUN-2001; 2001US-302051P
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                                                                                                                                                                                                                                                                Sequence 439 BP; 141 A; 99 C; 93 G; 106 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                        Note: With the exception of SEQ ID No 1 and 2, the sequence data
                                                                                                                                                                                                                                                                                                                                                                                                     proteins of the invention.
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                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                    patent did not form part of the printed specification but was by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID No 689; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meagher MJ,
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RESULT 10
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AB056306 to AB060787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78993 to ABB79004 represent proteins encoded by the AB060776 to AB060787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and for detecting the presence or absence of a polynucleotide encoded by a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I), and for determining the phenotype of cells in a sample of cells from a patient. (I) is useful for determining the presence or state of other type of cancer, in antisense therapy, to generate macroarrays on a solld surface, to identify a chromosome on which the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid that is differentially expressed in tissues useful for determining the presence of colon cancer in or tissue type, and in antisense therapy -
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c analysis; diagnostic; antisense therapy; gene; ss.
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n A, Lewis
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RESULT 11
ABV49231
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                                                                                   17-FEB-2000;
16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                             WO200160860-A2
                                                                                                                                                                                                                                                                               pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibodies, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             analysis, mapping and diagnostic applications. (I)
                                   Schlegel R,
                                                                                                                                                                                                      23-AUG-2001
                                                                                                                                                                                                                                                                                           Human; prostate cancer; cytostatic; carcinogen;
                                                                                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                                                                                              17-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                       ABV49231;
                                                                                                                                                                                                                                                                                                                                                                                             ABV49231 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        corresponding gene resides, and in tissue profiling, forensics,
                                                                                                                                                                             20-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              662 AAGTGTACCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACAT 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCAAGGCCCACGAGGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGG 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCTGTGGCAAAACA-TTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACGGAACTTCTGAAACATGTGAGAGAAACCCATAAAGAGGGAAATACTATGTGAAGTATGC 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAAGGTCCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACAT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGAAAACATTTAAACGCAAAGATTACCTTAAGCAACACATGAAAACTCATGCCCCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGAAAACATTTAAACGCAAAGATTACCTTAAGCAACACATGAAAACTCATGCCCCAGAA 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCAAGGCCCACGAGGGCTATGTATGTCAAAAAAGGATGTTCCTTTGTGGCAAAAACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCTGTGGCAAAACATTTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCCAAAGCCATATCCTCCTTCCATGAGGAAAGCCCGCCTTTTTNGTGTGAACATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGGATGTATGTCGCTGTCCAAGANAAGGCTGTGGAAGAACCTAT - CAACTGTGTTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGGATGTATGTCGCTGTCCAAGAGAAGGCTGTGGAAGAACCTATACTACTGTGTTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGGAACTTCTGAAACATGTGAGAGAAACCCCATAAAGAGGAAATACTATGTGAAGTATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402;
                                                                                                                                                                                                                                                                                                                    prostate expression marker cDNA 49222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                             MILLENNIUM PREDICTIVE MEDICINE
                                                                                   2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
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                                  Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 196 A; 116 C; 106 G; 117 T; 2 other;
                                                                                                                                                                             2001WO-US05171
                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                             marker; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to screen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.4%;
96.6%;
                                                                                                                                                                                                                                                                                                                                                                                              466
                                   Monahan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for peptide analogues and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 374; DB; Pred. No. 1.4e; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .4e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 24;
                                                                                                                                                                                                                                                                                           pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               can be used to raise
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WPI; 2001-662795/76

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RESULT 12
ABV19459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid molecule (I) com a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of t specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient (f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful
                       23-AUG-2001
                                                                                                                                                           13-SEP-2002
                                                                                                                                                                                                            ABV19459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
20-FEB-2001; 2001WO-US05171
                                               WO200160860-A2
                                                                                              pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        patient;
                                                                                                                                                                                                                                                                                                1037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATGTGAGAGAAACCCATAAAGAGGAAATACTATGTGAAGTATGCCGGGAAAACATTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGGACGGAACTTCTGAAA 796
                                                                                                                                                                                                                                                                                                TTT
                                                                                                                                                                                                                                                                                                                     TGTCCAAGAGAAGCTGTGGAAGAACCTATACAACTGTGTTTAATCTCCAAAGCCATATC
                                                                                                                                                                                                                                                                                                                                                                                                                               TTT
                                                                                                                                                                                                                                                                                                                                            TGTCCAAGAGAAGGCTGTGGAAGAACCTATACTACTGTGTTTAATCTCCAAAGCCATATC
                                                                                                                                                                                                                                                                                                                                                                                                                     CATGTGAGAGAAACCCATAAAGAGGAAATACTATGTGAAGTATGCCGGAAAACATTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAAACATGGACGGAACTTCTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302;
                                                                                                                                   prostate expression marker cDNA 19450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             also
                                                                                                           prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466
                                                                                                                                                                                                                                                                                              1039
                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                        466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 9624; 11750pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP;
                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  presence of prostate cancer, stage
                                                                                                           cancer;
                                                                                               marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153
                                                                                                                                                                                                           CDNA;
                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.7%;
99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Α.
                                                                                              cytostatic;
gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 C; 102 G; 119 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmacodyanamic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 301.4; DB 2
Pred. No. 1.2e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English
                                                                                                                                                                                                           ВΡ
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                                                                                                        carcinogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                          pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 466;
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                                                                                                                                                                                                                                                                                                                                             1036
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RESULT 13
AAH22129/c
ID AAH22
XX
AC AAH22
XX

AAH22129 standard;

CUNA:

2

AAH22129

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cc a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the cc specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate

CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer

CC (a) assessing the efficacy of a therapy for inhibiting prostate cancer

CC (e) selecting a composition for inhibiting prostate cancer in a patient

CC (f) assessing the prostate cell carcinogenic potential of a compound:

CC (h) assessing the addressivence.
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Best Local
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                        1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, usef for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                         Sequence 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                               patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-)
424
                                                   364
                                                                             977
                                                                                                      304
                                                                                                                                917
                                                                                                                                                         244
                                                                                                                                                                                     857
                                                                                                                                                                                                             184
                                                                                                                                                                                                                                         797
                                                                                                                                                                                                                                                                  124
                                                                                                                                                                                                                                                                                                                                                                                                                       selecting a composition for inhibiting prostate cancer in a patien assessing the prostate cell carcinogenic potential of a compound: determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of professions.
                                                                                                                                                                                                                                                                                                                                                                                                 is also useful as a pharmacodyanamic or pharmacogenomic
3-
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                                                             TGTCCAAGAGGAGGCTGTGGAAGAACCTATACTGTGTTTTAATCTCCAAAGCCATATC
                                                                                                                                                         CATGTGAGAGAAACCCATAAAGAGGGAAATACTATGTGAAGTATGCCGGAAAACATTTAAA
                                                                                                                                                                                                                                                                            GGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGGACGGAACTTCTGAAA
                                                                                                                                                                                  CATGTGAGAGAAACCCATAAAGAGGAAATACTATGTGAAGTATGCCGGAAAAACATTTAAA
                                                                                                                                                                                                                                                                GGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGGACGGAACTTCTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-662795/76
                                                   TGTCCAAGAAAGGCTGTGGAAGAACCTATACAACTGTGTTTAATCTCCAAAGCCATATC
                                                                                                                                                                                                                                                                                                                      301;
                        1038
                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-2119007P.
2000US-255281P.
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                         BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endege
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3184; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                       142 A;
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                                                                                                                                                                                                                                                                                                                                23.68;
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                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                             Score 300.4;
                                                                                                                                                                                                                                                                                                                                  Pred
                                                                                                                                                                                                                                                                                                                                                                         90 G;
                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                  No.
                                                                                                                                                                                                                                                                                                                                                                         114 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INC
                                                                                                                                                                                                                                                                                                                                  2e-68;
                                                                                                                                                                                                                                                                                                                                                                         0 other;
                                                                                                                                                                                                                                                                                                                                               DΒ
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heIF3;
                                                                                                        1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a human eukaryotic initiation factor (cIF), designated heIF3), which is expressed in human dendritic cells. heIF3 has translation initiation factor activity. Also described in the present invention are methods for the preparation and detection of the heIF3 protein and nucleotide sequences. The present sequence encodes heIF3, as given in the present invention.
                                                                                                                                                                                                                                                                                                                        1401 GGCAAAACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTTGTTGTACATGATCCTGAC 1342
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                                     AAS73534 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1401 BP; 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human translation initiation factor protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-282654/30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUN-2000; 2000CN-0116791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JUN-2000; 2000CN-0116791
                                                                                                                                                                                                                                                                                                                                                                          Local Sinhes 246;
                                                                                                                                                                                                                              CTCAGTGGATATATCCCTCCCAAAAGGAAACAAGGGCAAGGCTTATCTTTGTGTCAAAAC
                                                                                                                                                                                                                                                                                  AAGAAGAAATGAAGCTCAAAGTCAAAAATCTCGTGAAAAAACGGAGTTTGGCCTCTCAT
                                                                                                       GGCTAA
                                                                                                                                                                                   GGAGAGTCACCCAACTGTGTGGAAGACAAGATGCTCTCGACAGTTGCAGTACTTACCCTT
                                                                                                                                                                                                               CTCAGTGGATATCCCTCCCAAAAGGAAACAAGGGCAAGGCTTATCTTTGTGTCAAAAC
                                                                                                                                                                                                                                                                   AAGAAGAAATGAAGCTCAAAGTCAAAAATCTCGTGAAAAACGGAGTTTGGCCTCTCAT
                                                                                                                                                                                                                                                                                                                                                GGCAAAACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGATCCTGAC 1087
                                                                                                                                 GGCTAA 1273
                                                                                                                                                           GGAGAGTCACCCAACTGTGGGAAGACAAGATGCTCTCGACAGTTGCAGTACTTACCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eIF3; eukaryotic initiation factor; translation initiation factor;
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 17 (disclosure);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xiao H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                     cDNA; 1889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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1166 CCCAAAAGGAAACAAGGGCAAGGCTTATCTTTGTGTCAAAACGGAGAGTCACCCAACTGT 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No 9338; 103pp; English
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                                                                                                                                                                                                                                                                                                                                       Sequence 1889 BP; 488 A; 453 C; 417 G; 531 T;
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les 275; Conser
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                                  AAACCAAGTCTCACTAGCGATGCTGTTGTACATG-TCCTGGCAAGAAGAAAATGAAGCTC
                                                                                                                                                                                       CATGAGGAAAACCGCCCTTTTGTGTGTGAACATG~TGGCTGTGGCAAAACA~TTGCAAAT 59
                                                                                                                                               AAACAAAGTCTCACTAGGCATGCTGTTGTACATGATCCTGACAAGAAGAAAATGAAGCTC 1105
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                                                                                                                  Query Match
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Matches 234
                                                                                                                                                                                                                                                                  The invention relates to polynucleotides encoding colon tumour proteins. The polynucleotides and encoded polypeptides are useful in pharmaceutical compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polynucleotide sequences may be used as hybridisation probes or primers, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating an immune response against cancer, particularly for the immunotherapy of colon cancer, and as markers for the progression of cancer.
                                                                                                                                                                                                            proteins of the invention.

Note: With the exception of SEQ ID No 1 and 2, the sequence data for this pattent did not form part of the printed specification but supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-2000; 2000US-223283P
28-MAR-2001; 2001US-279763P
29-JUN-2001; 2001US-302051P
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 610; 147pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New colon cancer polypeptides and polynucleotides, useful as vaccines, for diagnosing, preventing, and treating colon cancer, and as markers
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              680 TGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACATGCCAAGGCCCACGAGGGC 739
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                                                       the progression of cancer
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                                                                                                                18.4%; Score 234; DB 24; Length 234; 100.0%; Pred. No. 3.3e-51; vative 0; Mismatches 0; Indels
                                                                                                                                                                             A; 50 C; 53 G; 48 T; 0 other;
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Search completed: February 10, 2003, 12:56:10 Job time: 308.842 secs



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1: /cgn2_6/ptcodata/2/pna/PGT_NEW_COMB.seq:*

2: /cgn2_6/ptcodata/2/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptcodata/2/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptcodata/2/pna/US09_NEW_COMB.seq:*

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GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative sp.

FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: U$/09/724,676

CURRENT FILLING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: PatentIn version 3.2

SEQ ID NO 44689

LENGTH: 1906
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                                                                                                                                                                                                                                                                                                                                                   LENGTH: 19
                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens FEATURE:
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US-09-724-676A-44614
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Scoring table:

Title: Perfect score:

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RESULT 2
US-09-724-676A-44689
Sequence 44689, App
GENERAL INFORMATION
APPLICANT: Compuge:
TITLE OF INVENTION
FILE REFERENCE: 12:
CURRENT APPLICATION
Sequence 44689, Application US/09724676A GENERAL INFORMATION:

APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION NUMBER: US/09/724,676A
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1814)..(1814)
; OTHER INFORMATION: n is a
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Best Local Sim
Matches 1270;
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NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 44689
LENGTH: 1906
TYPE: DNA
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                                       TGCCAAGGCCCACGAGGCTATGTATGTCAAAAAGATGTTCCTTTTGTGGCAAAAAACATG
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Sequence 44634, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spl
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
UNUMBER OF SEO ID NOS: 97222
SOFTWARE: Patenth version 3.2
SEQ ID NO 44634
LENGTH: 2019
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
LOCATION: (1927)..(1927)
OTHER INFORMATION: n is a,c,9, or t
US-09-724-676-44634
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US-09-724-676-44634
Sequence 44634, App.
GENERAL INFORMATION
APPLICANT: COMPUNG
TITLE OF INVENTION
FILE REFERENCE: 11.
CURRENT APPLICATION
CURRENT FILING DAY
NUMBER OF SEO ID NO 44634
INVENTAL 2019
TYPE: DNA
ORGANISM: HOMO SE
FRATURE:
NAME/KEY: misc_fe
NAME/KEY: misc_fe
LOCATION: (1927)
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                                                TCAAAACGGAGAGTCACCCAACTGTGTGGAAGACAAGATGCTCTCGACAGTTGCAGTACT
                                       ACGTGTCTCGGCACGTGGCAGCGCGCCTGGCCCTGGGCTTGGAGGCGCCGGCGCCCTGGA
                                                                             Conservative
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                    TACCCTTGGCTAA 1273
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1927)...(1927)
; OTHER INFORMATION: n is a.c.g. o
US-09-724-676A-44634
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative sp
FILE REFERENCE: 12918.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SED ID NOS: 97222
SOFTWARE: Patentin version 3.2
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                                                                                                                       Query Match 99.6%;
Best Local Similarity 99.8%;
Matches 1270; Conservative
                                                                                                                                                                                                  SEQ ID NO 44645
LENGTH: 2104
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEO ID NOS: 97222
SOFTWARE: Patentin version 3.2
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                                GTGCCGGCGCGCGAAGGTTCAGCAGGGAGCCGTGGGCCGGGCGCGCCGGTTCCCGGC
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          TCAAAACGGAGAGTCACCCAACTGTGTGGAAGACAAGATGCTCTCGACAGTTGCAGTACT
                                                        CTCTCATCTCAGTGGATATATCCCCTCCCAAAAGGAAACAAGGGCAAGGCTTATCTTTGTG
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                                              CTCTCATCTCAGTGGATATATCCCTCCCAAAAGGAAACAAGGGCAAGGCTTATCTTTGTG
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; ORGANISM: Homo sapiens
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US-09-724-676A-44645
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 44645
LENCTH 2104
TYPE: DNA
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TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
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APPLICANT: Compugen LTD
ITTLE OF INVENTION: Variants of alternative sp
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTMARE: PatentIn version 3.2
SEQ ID NO 44678
SEQ ID NO 44678
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-676-44678
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US-09-724-676-44678
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US-09-724-676A-44678

Sequence 44678, Application US/09724676A

GENERAL INFORMATION:
APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 44678

LENGTH: 2239

TYPE: DNA
ORGANISM: Homo Sapiens
US-09-724-676A-44678
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 CAAGTGTACCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACA
                           CTTTAAGAAACATCAGCAGCTGAAAATCCATCAGTGCCAGCATACCAATGAACCTCTATT
                                                                                          ACGCAAACATGAAAATCAACAAAAACAATATATGCAGTTTTGAAGAGCTGTAAGAAGAC
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                                                                              ACGCAAACATGAAAATCAACAAAAACAATATATGCAGTTTTGAAGACTGTAAGAAGAC
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                                                                                                                                                             SEQ ID NO 44656
LENGTH: 2271
TYPE: DNA
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                                                                                           Matches
                                                                                                    Query Match
Best Local
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                                                                                                                                                                                           APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative .
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEO 1D NOS: 97222
SOFTWARE: Patentin version 3.2
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                                                                                           Conservative
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TCAAAACGGAGAGTCACCCAACTGTGGGAAGACAAGATGCTCTCGACAGTTGCAGTACT
                                                 CTCTCATCTCAGTGGATATATCCCTCCCAAAAGGAAACAAGGGCAAGGCCTTATCTTTGTG
                                                                                             GACGGAACTTCTGAAACATGTGAGAGAAACCCATAAAGAGGAAATACTATGTGAAGTATG
                              TCCTGACAAGAAGAAAATGAAGCTCAAAAGTCAAAAAATCTCGTGAAAAAACGGAGTTTGGC
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LENGTH: 2271
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TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEO LD NOS: 97222
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo
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Pred. No. 0;
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Sequence 44623, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative sp
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEO ID NOS: 97222
SOFTWARE: Patentin version 3.2
LENGTH: 2352
TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 44623, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spiritle Reference: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEO ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEO ID NO 44623
LENGTH: 2352
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-676A-44623
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Matches 1270; Conserv
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LENGTH: 2384
TYPE: DNA
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                                                                                    Matches 1270;
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Best Local (
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
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US-09-724-676A-44601
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TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
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Sequence 44667, Application US/09724676

GENERAL INFORMATION:
APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative spl
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: 05/09/724.676

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 44667

LENGTH: 2536

TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-676-44667
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Db 1160 CTCTCATCTCAGTGGATATATCCCTCCCAAAAGGAAACAAGGCCTAACCTTTTCTG 1219

Oy 1201 TCAAAACGGAGAGTCACCCCAACTGTGTGAAAGACAAGGCCTCTCGACAGTTCCT 1260

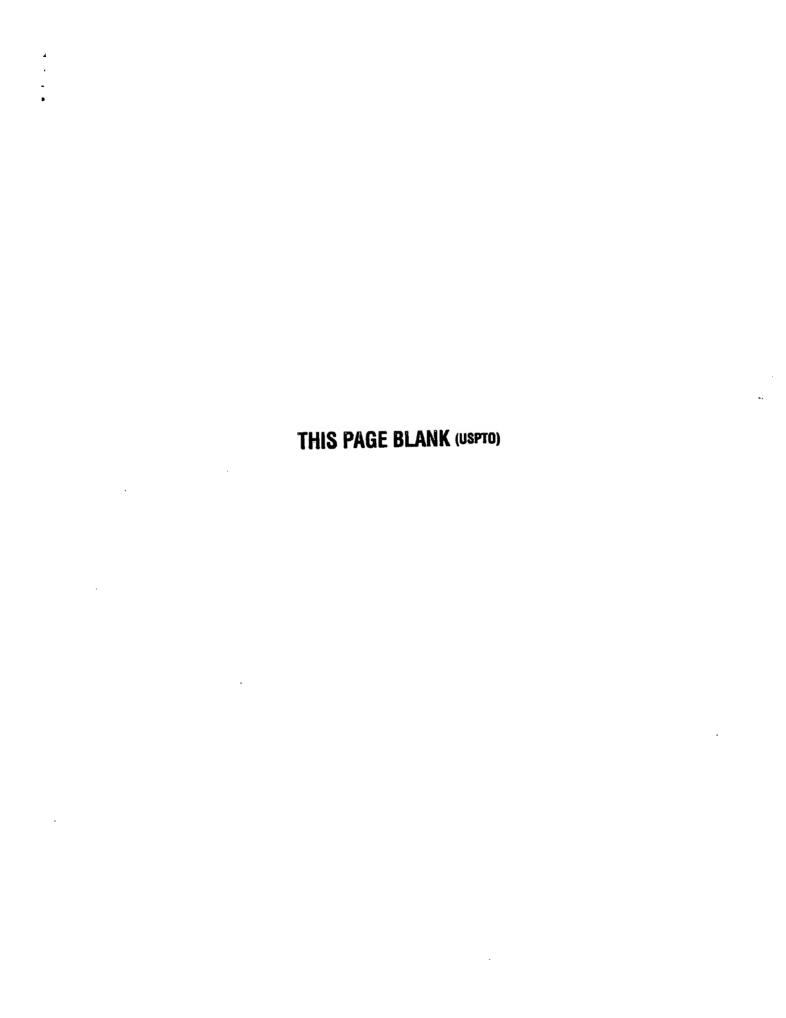
Db 1220 TCAAAACGGAGAGTCACCCCAACTGTGTGGAAGACAAGATGCTCTCGACAGTTGCAGTACT 1279

Oy 1261 TACCCTTGGCTAA 1273

Db 1280 TACCCTTGGCTAA 1292

Search completed: February 10, 2003, 13:05:19

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## SUMMARIES

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## ALIGNMENTS

REFERENCE AUTHORS		ORGANISM	COCKCE	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	RESULT 1 HUMIIIA
1 (bases 1 to 1381) Arakawa,H., Nagase,H., Hayashi,N., Ogawa,M., Nagata,M.,	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	and Y. Nakamura clone: 39Hll.	Homo saniens cons to man clone libilibrarry of T sullwara s shin	GTF3A; Xenopus transcription factor IIIA homologue.	D32257.1 GI:1000446	D32257	complete cds.	scription	HUMIIIA 1381 bp mrNA linear PRI 07-FEB-1999	

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                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-JUL-1994) Yusuke Nakamura, Cancer Institute, Department of Biochemistry; 1-37-1 Kami-Ikebukuro, Toshima Tokyo 170, Japan (E-mail:nakamura@ganvx1.jfcr.or.jp, Tel:03-3918-0111(ex.4501), Fax:03-3918-0342)
Location/Qualifiers
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VERSION KEYWORDS SOURCE ORGANISM

Homo sapiens Eukaryota; Metazoa; Homo sapiens.

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1399)
Fujiwara, T., Takeda, S., Shimada, Y., Ozaki, K. and Shi HUMAN TRANSCRIPTIONAL FACTOR 111A GENE Patent: JP 1996070870-A 1 19-MAR-1996;

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Pred. No. 9.2e
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1289. .1399.
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                 2 (bases 1 to 1173)
Becker, K.G.
Direct Submission
Submitted (25-JAN-1995) Kevin G. Becker,
Diseases and Stroke/NIH, Neuroimmunology
Pike, Bethesda, MD 20892, USA
Pike, Bethesda, MD 20891, USA
1, .1173
                                                                                                                                                                            Gene 159
95347600
                                                                                                                                                                                                          Cloning and expression Xenopus TFIIIA
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/organism*"Homo sapiens"
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                           CGCAAACATGAAAATCAACAAAAACAATATATATGCAGTTTTGAAGACTGTAAGAAGACC
                                                         GCAGCCAATGGCTGTGATCAAAAATTCAACACAAAATCAAACTTTGAAGAAACATTTTGAA
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829. .
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565. 631
/note="encodes zinc-finger"
649. 709
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208. .
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/protein_id="AAA75623.1"
/protein_id="AAA75623.1"
/db_xref="GI:644871"
/tanslation="PPAVAESVSSLTIADAFIAAGESSAPTPPRPALPRRFICSFPD
/sanyskawkldahlckhtgerPfyCDYEGCGKAFIRDYHLSRHILTHTGEKPFYCAA
GCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTEKKHQQLKIHQCQHTNEPLF
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VCRKTFKRKDYLKQHMKTHAPERDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFV
CEHAGCGKTFAMKQSLTRHAVVHDPDKKKMKLKVKKSREKRSLASHLSGYIPPKRKQG
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Accession Number P03001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="female"
/tissue_type="brain; hippocampus"
/clone_lib="stratagene #936205"
/dev_stage="2 years old"
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484. .550
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394. .460
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298. .367
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/clone="C2H2-34.10"
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283 c 265 g 262 t
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Pred. No. 1.5e-227;
0; Mismatches 2;
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                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1098)
Drew,P.D., Nagle,J.W., Canning,R.D., Ozato,K., Biddl Becker,K.G.
                         Direct Submission

Submitted (29-AUG-1994) Kevin G. Becker, Netional Institute
Neurological Diseases and Stroke/NIH, Neuroimmunology Branch
Rockville Pike, Bethesda, MD 20892, USA
                                                                                 Becker, K.G.
                                                                                                            Unpublished
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661. .732
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/protein_id="AAA21873.1"
/db_xref="GI:551535"
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/tissue_type="brain"
/clone_lib="Human hippocampus cDNA library, Stratagene
Number 936205"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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                                     Homo sapiens
                                                               Oligo capping; fis (full insert : Homo sapiens stomach mucosa cDNA
                                                                                                                    AKU57993 1920 bp Homo sapiens cDNA FLJ25264 fis, TRANSCRIPTION FACTOR IIIA.
                                                   clone:STM05057.
                                                                                           AK057993.1 GI:16553988
                                                                                                            AK057993
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           Eutheria;
             Chordata;
Primates;
           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                               A to mRNA,
                                                                                                                                  mRNA linear
clone STM05057, his
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                                                                                                                                  highly similar to
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Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S., Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiguchi,S., Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M., Yamashita,H., Chiba,Y., Suzuki,Y., Hata,H., Nakagawa,K., Wizuno, Morinaga,M., Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato, Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and Sugano,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA ilbrary construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.
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Direct Submission
Sumic G24-CCT-2001) Sumio Sugano, Institute of Medical Scia
Submitted (24-CCT-2001) Sumio Sugano, Institute of Medical Scia
University of Tokyo, Laboratory of Genome Structure, Human Genc
Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:cdnal@ims.d-tokyo-ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
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2 (bases 1
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/db_xref="taxon:9606"
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/tissue_type="stomach mucosa"
/clone_lib="STM"
/clone_lib="STM"
/note="cloning vector: pME18SFL3"
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                                                                                                                                                                                                                                                                               of Oklahoma Health Science Center,
Oklahoma City, OK 73104, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    Submitted (14-JUN-2001) Biochemistry/Molecular Biology, University of Oklahoma Health Science Center, 800 Research Parkway, Suite 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanas,J.S., Hocker,J.R., Cheng,Y.G., Lerner,M.R., Brackett,D.J., Lightfoot,S.A., Hanas,R.J., Madhusudhan,K.T. and Moreland,R.J. Coning, DNA binding, and evolution of mammalian transcription
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nas.J.S., Hocker,J.R., Lerner,M.R., Brackett,D.J.,
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           GTTGTACATGATCCTGACAAGAAGAAAATGAAGCTCAAAGTCAAAAATCTCGTGAAAAA
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Hanas,J.S., Hocker,J.R., Lerner,M.R., Brackett,D.J.,
Lightfoot,S.A., Hanas,R.J., Maduhadson,K. and Moreland,R.J.
Direct Submission
Submitted (14-JUN-2001) Biochemistry/Molecular Biology, University
of Oklahoma Health Science Center, 800 Research Parkway, Suite 448,
Oklahoma City, OK 73104, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus transcription AF391798
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21673987
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Hanas, T.S., Hocker, J.R., Cheng,
Lightfoot, S.A., Hanas, R.J., Mac
CDNA cloning, DNA binding, and
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Mammalia; Eutheria;
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CPREGCARTYTTYFNLQSHILSFHEEKRPFYCEHAGCGKTFAMKQSLWRHSYVHDPDK
KRMKLKVRPPRERRSLASRLSGYVPPKGKQEPDCSLPNSTESSSSPEATMLAPAALLT
                                                                                                                                                                                                           /translation="AARAGALPSRFTCSFPDCSASYNKAWKLDAHLCKHTGERSFVCDYEGCGKAFIRDYHLSRHILIHTGEKPFVCADNGCNQKFSTKSNLKKHIERKHENPQKQYCNFEGCKKAFKKHQQLRTHQCQHTNEPLFRCTHEGCGKHFASPSRLKRHGKVHEGYY
                                                                                                                                                                                                                                                       /product="transcription
/protein_id="AAL69685.1"
/db_xref="GI:18448380"
                                                                                                                                                                                                                                                                                                                  /note="TFIIIA; Cys2His2 zinc Xenopus laevis transcription Accession Number P03001"
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/db_xref="taxon:10116"
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J., Madhusudhan, K.T. and Moreland, R.
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IMAGE:5374268,
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                                                                                                GCCTTCATCAGGGACTACCATCTGAGCCGCCACATTCTGACTCACACAGGAGAAAAGCCG
                                                     GCCTTCATCAGAGACTACCATCTGAGCCGGCATGTCCTGATTCACACCGGGGAAAAGCCG
                                                                                                                                                   681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N. Ayele,K. Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W. Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighl,P.,
Hansen,N., Ho,S.-t., Karlins,E., Kwong,P., Laric,P., Legaspi.R.,
Maduro,O.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramury
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLML at: http://lmage.llr. Series: IRAK Plate: 65 Row: 1 Column: 4
This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (06-JUN-2002) National Institutes of Hee
Gene Collection (MGC), Cancer Genomics Office, Nat
Institute, 31 Center Drive, Room 11A03, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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/translation="Mgktwfellkhmreahkeditcnvcormfkrrdylkohmkthap
/translation="Mgktwfellkhmreahkeditcnvcehagggktfamkoslmhrsv
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/yhdddkkhmklkvraprerrslasrlsgyfppkrkgepdyslpnasaesssspeaglp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Mammary tumor.old mouse. Taken by biopsy."
                                                                                                                                                                                                                                                                                                                                                                                                      /product="general transcription
/protein_id="AAH32292.1"
/db_xref="GI:21595508"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_Mam2"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /map="FVB/N-3"
/clone="MGC:40923 IMAGE:5374268"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Vector: pCMV-SPORT6"
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/db_xref="taxon:10090"
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AC004739
Submitted (23-MAY-1998)
                                                               unpublished
                                                                               The sequence of Homo sapiens
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                 Direct Submission
                                   Waterston, R
                                                                                                 Kemp
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Department of Genetics,
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AUTHORS
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                                                                                                                      Submitted (03-FEB-2000) Department of Genetics, University, 4444 Forest Park Avenue, St. Louis,
                                                                                                                                                            Waterston, R.
Direct Submission
                                                                                                                                                                                               University,
3 (bases 1
Center project name: H_DJ0531G15
                                Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                      Center code: WUGSC
                                                                                     Center: Washington University Genome
                                                                                                                                                                                               4444 Forest Park Avenue,
to 97979)
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                                                                                                                                                                                                                Louis, Missouri 63108, USA
                                                                                                                          Missouri
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                                                                                                                            63108,
                                                                                                                            USA
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COMMENT

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problem such as compressions and repeats; all regions were covered by sequence from more than one subcione; and the assembly was confirmed by restriction digest. problems

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc and

# SOURCE INFORMATION:

The actual start of this clone is at base position 1 of RP4-531G15, actual end is at base position 97979 of RP4-531G15. 6:84-9 (1994). The library is from one male donor. details, see http://bacpac.med.buffalo.edu/
The clone is available from Genome Systems, Inc. This clone was derived from human PAC library RPCI-4, prepared Pieter de Jong and coworkers at Roswell Park Cancer Institute, using the method described by Ioannou et al., Nature Genetics The actual start of this clone NEIGHBORING SEQUENCE INFORMATION: (http://www.genomesystems.com). PCYPAC2 For further prepared ρy

FEATURES source repeat\_region repeat\_region repeat\_region repeat\_region This clone contains STS swSS2758 (NID:glll13567) /rpt\_family="L2" 660. .831 /rpt\_family="Alu" 3868. .4067 /rpt\_family="Alu" 137. .179 /map-"7p21" /db\_xref="taxon:9606" /chromosome="7" 1. .62 /clone\_lib="RPCI-4" /clone="RP4-531G15" /organism="Homo sapiens' Location/Qualifiers \_family="MIR"

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complement(3358. 33668)

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                                               AAATTATATGTCAATAGGGATGTTCTTTTGTGGCAGAAACATGGAC------
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                                                             Local Similarity
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HTG.
                                                                                                                                                                                      University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On May 5, 1999 this semience ......
                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (22-NOV-1998) Genome
University School of Medicine,
                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                  io 63108, USA
In May 5, 1999 this sequence vocation/qualifiers
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Mammalia; Eutheria; Primates;
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The sequence of Homo saplens BAC clone RP11-515K14
Unpublished (2001)
3 (bases 1 + 417...
                                                                                                              Direct Submission
Submitted (21-FEB-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 6
On Jan 19, 2002 this sequence version replaced gi:17976493
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Submitted (30-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Waterston, R.
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web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
Center project name: H_NH0515K14
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions. NOTICE:

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality and the covered quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Mashington University), and the Mashington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/CTB/CHR7, send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is CTD-2105K18, 2000 bp overlap; the clone sequenced to the right is RF11-533K11, 2000 bp overlap. Actual start of this clone is at base position 141753 of CTD-2105K18; actual end is at base position 16829 of RF11-533K11.

Polymorphisms have been identified between AC016444 and AC074390

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Pred. No. 3.5e-88;
                                                                                                                                                                                                                                                                                                                                                                       Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                               DB 9;
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                                                                                                                                                                                     Baldwin, J. Barna, N. Beckerly, R. Boguslavkiy, L. Boukhgalter, B. Brown, A., CastLe, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hayos, B., Heaford, A., Horton, L., Galagan, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Hewald, J.C., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Margun, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
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1 (bases 1 to 20622)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                              On Sep 9, 2000 this sequence version replaced gi:6778507 All repeats were identified using RepeatMasker: smit, A.F.A. & Green, P. (1996-1997)
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206622 bp

Homo sapiens chromosome 11 clone
SEQUENCE, 16 unordered pieces.
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                 Submitted (26-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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* This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58236 56952: contig of 11357 bp in length 69593 69592: gap of 100 bp 69693 80894: contig of 11142 bp in length 80835 80934: gap of 100 bp 80935 102411: contig of 21477 bp in length 102412 102511: gap of 100 bp 102512 127924: contig of 25413 bp in length 127925 128024: gap of 100 bp 126326 156338: contig of 34314 bp in length 126326 156338: contig of 34314 bp in length 166326 166326 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626 25626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project Information Center project name: L5006 Center clone name: 384_I_14
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Insert size: 205122; sum-of-contigs
Quality coverage: 4.2 in Q20 bases; agarose-fp
Quality coverage: 4.4 in Q20 bases; sum-of-contigs
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162439 206622: contig of 44184 bp in length
Location/Qualifiers
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48160 58135; contig of 9976 bp in length
58136 58235; gap of 100 bp
58236 69592; contig of 11357 bp in length
69593 69692; gap of 100 bp
69693 80834; contig of 11142 bp in length
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48160 581
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13593. .14758
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14859. .16187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2/333: contig of 4688 bp in length
33: gap of 100 bp
32718: contia ~f 77
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Best Local Similarity 80.3%;
Matches 685; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36308 CCCCTTCACACACTTCTTAGGAGGGTCATCTGCTACTTCCC-CAGTGTGGCACCACTTAC 36366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36367 AAAAAGGCCTGGAAGCTTAATGTGCACCTGT--AATCACATGGGGAAGAAACCATTTGTT
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GAGAGAAACCCATAAAGAGGAAATACTATGTGAAGTATGCCGGAAAAACATTTAAACGCAA 861
                                                                   TATATGTCAAAAAGCGTGTTCTTTTGTGGTGAAAGCATGAACAGAAGTTTTGAAACATGT
                                                                                                                                                                                                                                                             TGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACATGCCAAGGCCCACGAGGGCTA 741
                                                                                                                                                                                                                                                                                                                                                                        A-----ATATATATGCAGTTTTGAAGACTGTAAGAAGACCTTTAAGAAACATCAGCAGCT 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCAACACAAAATCAAACTTGAAGAGACATTTTACAGGCAAACATGAAAACCAGCAAAAAA 36603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCAACACAAAATCAAACTTGAAGAAACATTTTGAACGCAAACATGAAAAATCAACAAAAAC 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTGA-TCATACTGCAGACAAGCCATATGTTTGTGCAGCTAGTAGCTGTGATCTAAAAAT 36543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTGACTCACACAGGAGAAAAGCCGTTTGTTTGTGCAGCCACTGGCTGTGATC-AAAAAT 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATGACTGTGAAGGGTGTGGCAAGACCCACCTCAAGAGACTAACATCTGAGTTGTCATGT 36484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTGACTATGAAGGGTGTGGCAAGGCCTTCATC-AGGGACTACCATCTGAGCCGCCACAT 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCAAAGCCTGGAAGCTTGACGCGCACCTGTGCAAGCACACGGGGGGAGAGACCATTTGTT 388
                                                                                                                            TGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGGACGGAACTTCTGAAACATGT 801
                                                                                                                                                                                                                                                                                                                                    GAAAAACCATCACTGCCAGCATACCAATGAACCACTATTCAACTGTACCCAGGAAAGATG
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                                                                                                                                                                                                    TGGGAAGCATTTTTCCCCCATCCATCCAGC-----AAGCGGCAAGGCCCATGCGGGCTC
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69693, .80834
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48160. .58135
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18729. 22545
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16288. .18628
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102512. .127924
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27434. .32718
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This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Jan 28, 2001 this sequence version replaced gi:12580980.
During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                          Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9 RPII-575C20 is from the library RPCI-11.2 constructed of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                           http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
This sequence is the entire insert o
                                                                                                                                                                                                                                                                                                                                    Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 199517)
                                                               sequence is the entire insert of clone RP11-575C20 The true end of clone RP11-279E1 is at 116738 in this sequence. The right end of clone RP11-21817 is at 84470 in this sequence.
∕organism≖"Homo sapiens
                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from clone
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                   A-TATGGCAGAAAATTTTTAAACACAAAGATTATCTTAAGCAATATATGAAAACTCTTGC
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                                                                                                             TCCAGAGAGAATATTTGCCAATGTTCAAGAGAAGGCTGTGGTAGAACCCACATGACTGT
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restriction digest data."
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159090. .159136
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/chromosome="9"
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Pred. No. 6.4e-87;
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                                                                                         AAAATGAAGCTCAAAGTCAAAAAATCTCGTGAAAAAACGGAGTTTGGCCTCTCATCTCAGT 1153
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AX396474
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/db_xref="taxon:9606"
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Pred. No. 4.5e-81;
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TCACCCAACTGTGTGGAAGACAAGATGCTCTCGACAGTTGCAGTACCTTACCCTTGGCTAA 1273
                                                 GGATATATCCCTCCCAAAAGGAAACAAGGGCAAAGGCTTATCTTTGTGTCAAAACGGAGAG 1213
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Search completed: February 10, 2003, 16:50:50 Job time: 4126.18 secs

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### ALIGNMENTS

REFERENCE AUTHORS TITLE KEYWORDS SOURCE ORGANISM RESULT 1
BM553401
LOCUS
DEFINITION ACCESSION VERSION FEATURES COMMENT JOURNAL source Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1968 row: o column: 07

High quality sequence stop: 673. 1078
AGENCOURT\_6572564 NIH\_MGC\_41
5', mRNA sequence.
BM553401 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999) Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1078) EST Homo sapiens BM553401.1 GI:18792097 human. Location/Qualifiers .1078 bp mRNA linear EST 20-FEB-2002 Homo sapiens cDNA clone IMAGE:5467230 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. be

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/clone_lib="NIH_MGC_41"
/clone_lib="NIH_MGC_41"
/tlssue_type="amelanotic melanoma, cell line"
/tlssue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)" Site_1: XhoI; Site_2:
/note="Organ: skin; Vector: pOTB7: Adaptor:
/note="Organ: skin; Vector: pOTB7: Adaptor: pOTB7: p
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/db_xref="taxon:9606"
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                                                                                                                 Conservative
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                                                                                                                                                                                                  cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville. Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fullength.invitrogen.com" a 244 c 232 g 195 t 17 others
                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: brain; Vector: pCMVSPORT 6; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="CS0DA009Y018"
/clone_lib="LTI_NFL011_NBC1"
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/lab_host="DH10B"
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Genoscope - Centre National de Sequencage
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/db_xref="taxon:9606"
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Contact: Genoscope
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/note="vector: pcMvSPORT 6; Site_1: NotI; Ist strand cDNA
/note="vector: pcMvSPORT 6; Site_1: NotI; I and
cloned into the NotI and Eco RV sites of the pcMvSPORT 6
/vector: Library was normalized. Library was constructed by
/tife Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
/rockville, Maryland 20850, USA Fax: (1) 301 610 8371
// Email: filang@lifetech.com URL:
// http://fulllength.invitrogen.com"
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AGENCOURT_6588903 NIH_MGC_98
5', mRNA sequence.
BM562682
Unpublished (1999)
Contact: Robert Strausberg,
Email: cgapbs-r@mail.nih.gov
                                                                                           Homo sapiens
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GACCCCGCCGCGCCCCGCGCTTCCCAGGAGGTTCATCTGCTCCCTTCCCTGACTGCAGCGC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1059) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collec Homo sapiens cDNA clone **MRNA** Gene Collection Euteleostomi; EST 20-FEB-2002 MAGE:5478431

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="astrocytoma grade IV, cell line"
/lab_host="bH108 (phage-resistant)"
/note="Organ: brain; Vector: poTB7; Site_1: xhoI; Site_2:
/note="Organ: brain; Vector: poTB7; Site_1: xhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
pagetor: GCOCCONIXHO Sites using the following 5'
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/db_xref="taxon:9606"
/clone="IMAGE:5478431"
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                                                                                                                                                                       /clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="vector: pCMVSPORT 6; Site_l: NotI; lst strand cDNA
/note="vector: pCMVSPORT 6; Site_l: NotI; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
life Technologies. Contact: Feng Liang Life Technologies,
addition of Invitroms 0800 Madical Carter prime
                                                                                                                       a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliangelifetech.com URL:
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Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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BP 191 91006 EVRY cedex - F
Email: segref@genoscope.cns
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Contact: Genoscope
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segref@genoscope.cns.fr,
                                                     /note-*Organ: brain; Vector: pcMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:
                                 http://fulllength.invitrogen.com"
240 c 227 g 206 t
                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC024YE05"
                                                                                                                                                                                     /sex="male"
                                                                                                                                                                                                 /clone_lib-"LTI_NFL003_NBC3"
                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                           /tissue_type="neuroblastoma cells"
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/clone_lib="TrI_NFL006_PL2"
/tissue_type="placenta"
/tissue_type="placenta"
/note="Vector: pcWVSPORT 6; Site_1: NotI; Ist strand cDNA
/note="Vector: pcWVSPORT 6; Site_1: NotI; Ist strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcWVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Lieng Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filang@lifetech.com URL:
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AGENCOURT_6439143 NIH_MGC_71
BV5, mRNA sequence.
BM541851
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections (1988)
                                                                                                                                                                                                                                   CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information cal
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg,
                                                                                                                                                                                                      http://image.llnl.gov
Plate: LLAM12213 row: e column:
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/db_xref="taxon:9606"
/clone="IMAGE:5531503"
/clone_lib="NIH_MGC_71"
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/tlssue_type="lelomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_Site_2: Sall; Cloned unidirectionally. Primer: Average insert size 2.1 kb. "
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                                                                              GCTCCTTCCCTGACTGCAGCGCCAATTACAGCAAAGCCTGGAAGCTTGACGCGCACCTGT
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Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genomics@hri.co.jp
HRI human cDNA project; 5'. & 3'-end one pass sequencing:
Research Institute; cDNA library construction: Department
Virology, Institute of Medical Science, University of Toky
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1532-3 Yana, Kisarazu, Chiba
Tel: 81-438-52-3975
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/note="vector: pmE18sFt1"
/note="vector: 230 g 177 t
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/clone="HEMBA1002055"
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                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2484 row: j column: 14
High quality sequence stop: 642.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collegeratives (1800)
                                                                                                                                                                                                                                                                                                                                                  BQ644275
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EST.
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/clone_lib="NIH_MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
CCORI; cDNA made by oligo-dT priming. Directionally cloned
                                                               /clone="IMAGE:6285421"
                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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CDNA clone IMAGE:6285421
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into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript IRT (Life Technologies). Note: this is a NIH\_MGC Library."

GCTCCTTCCCTGACTGCAGCGCCAATTACAGCAAAGCCTGGAAGCTTGACGCGCACCTGT 359 CTGGCTGTGGCAAAACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATG 1079 GCCGGAAAACATTTAAACGCAAAGATTACCTTAAGCAACACATGAAAACTCATGCCCCAG CCTTTAAGAAACATCAGCAGCTGAAAATCCATCAGTGCCAGCATACCAATGAACCTCTAT CCTTTAAGAAACATCAGCAGCTGAAAATCCATCAGTGCCAGCATACCAATGAACCTCTAT GC-ANCACACGGGGGAGAGACCATTTGTTTGTGACTATGAAGGGTGTGGCAAGGCCTTCA GCAAGCACACGGGGGAGAGCCATTTGTTTTGTGACTATGAAGGGTGTGGCAAGGCCTTCA 419 GCTCCTTCCCTGACTGCAGCGCCAATTACAGCAAAGCCTGGAAGCTTGACGCGCACCTGT CCTCTCATCTCAGTGGATATAT-CCCTCCCAAAAGGAAACAAGGGCAAGG AAAGGGATGTATGTCGCTGTCCAAGAGAAGGCTGTGGAAGAACCTATACTACTGTGTTTTA 959 GGACGGAACTTCTGAAACATGTGAGAGAGAAACCCATAAAGAGGAAATACTATGTGAAGTAT ATGCCAAGGCCCACGAGGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACAT TCAAGTGTACCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGAC **AACGCAAACATGAAAAATCAACAAAAACAATATATGCAGTTTTGAAGACTGTAAGAAGA** AACGCAAACATGAAAATCAACAAAAAACAATATATATGCAGTTTTGAAGACTGTAAGAAGA ATCCTGACAAAAAG - AAATGAAGCTCCAAGTCCAAAAATCTCGTGAAAAACGGAGTTTGG ATCCTGACAAGAAAAATGAAGCTCAAAGTCAAAAATCTCGTGAAAAAACGGAGTTTGG CTGGCTGTGGCAAAACATTTGCCATGAAACAAAGTCTCACTANGCATGCTGTTGTACATG GGACGGAACTTCTGAAACATGTGAGAGAAACCCCATAAAGAGGAAATACTATGTGAAGTAT ATGCCAAGGCCCACGAGGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACAT TCAAGTGTACCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGAC <u>AAAGGGATGTATGTCGCTGTCCAAGAGAAGGCTGTGGAAGAACCTATACAACTGTTTTA</u> Similarity Conservative 65.7%; 0; Score Pred. Mismatches 836; No. 4. DB 1, 4.5e-173; 12; Length Indels 1188 ω •• Gaps 1019 479 429 599 539 189 70 848 729 669 609 899 549 839 489 779 719 369 659 309 249 ω

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TGGCAAAAACATGGACGGAACTTCTGAAACATGTGAGAGAAACCCCATAAAGAGGGAAATAC
                                   TGGCAAAAACATGGACGGAACTTCTGAAACATGTGAGAGAAACCCCATAAAGAGGAAATAC
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Contact: Genoscope
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/clone=lib="LTI_NFL006_PL2"
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/clone=lib="LTI_NFL006_PL2"
/clone=lib="LTI_NFL006_PL2"
/clone="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and end into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invirogen 9800 Medical Center Drive Book and Anna and Conter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rockville, Maryland 20850, USA Fax : (1) 301 610
Email : fliangelifetech.com URL :
http://fulllength.invitrogen.com"
192 c 207 g 326 t 6 others
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Pred. No. 8.3e-172;
4; Mismatches 7;
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5', mRNA sequence.
BQ278693
                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                       CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: breast; Vector: poTP; Site_1: EcoR
Site_2: XhoI: cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using
following 5' adaptor: GGCACGAG(G). Library const
                                                                                                    /clone="IMAGE:5805333"
/clone_lib="NIH_MGC_107"
                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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TCCAAAGCCATATC---CTCTCCCTTCCATGAGGAAAGCCGCCCTTTT---
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                                                                                                                                                                                                                                                                          908;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, |
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 927)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections
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Eukaryota; M
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602764826F1 NIH_MGC_42 Homo
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//db_xref="taxon:9666"
//clone_lib="NuAGE:4906710"
//clone_lib="NuAGE:4906710"
//clone_lib="NuH_MGC_42"
//tissue_type="epithelioid carcinoma cell line"
//lab_host="DHJDB (phage-resistant)"
//note="Organ: pancreas; Vector: pOTB7; Site_l: XhoI;
/note="Organ: pancreas; Vector: pOTB7; Site_l: XhoI;
/note="Organ: pancreas; Vector: pOTB7; Site_sing the
Directionally cloned into EcoRIX/NoI sites using the
following 5, adaptor: GCCAGGAG(G), Size-selected >500bp
for average insert size 1.8kb, Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
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110 US-09-783-590-544-3

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110 US-09-833-381-117-5

110 US-09-833-328-1747

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12 US-10-033-528-689

14 US-09-996-692-4064

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18 US-10-9395-973-2
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Sequence 68, Appli
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Sequence 1, Appli
Sequence 14, Appli
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Sequence 1747, Ap
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Sequence 689, App
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Sequence 4064, Ap
Sequence 610, App
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Sequence 119, App Sequence 119, App	Sequence 137, App Sequence 1716, Ap	Sequence 73, Appl	Sequence 120, App	Sequence 1613, Ap	Sequence 950, App	~	Sequence 4, Appli	Sequence 16, Appl	Sequence 642, App	Sequence 4925, Ap	Sequence 417, App	Sequence 211, App	Sequence 28, Appl	Sequence 17, Appl	Sequence 29, Appl	Sequence 1647, Ap	Sequence 4943, Ap	Sequence 76, Appl	Sequence 10, Appl	Sequence 2, Appli	Sequence 14, Appl	Sequence 14, Appl	Sequence 14, Appl

## ALIGNMENTS

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APPLICANT: King, Gordon E.

APPLICANT: Meagher, Madeleine Joy
APPLICANT: W. Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547
CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 326
LENGTH: 439
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US-09-920-300A-326/c
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Best Local Similarity
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Pred. No. 8.4e-103;
0; Mismatches 1;
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APPLICANT: King, Gordon E.

APPLICANT: Meagher, Madeleine Joy
APPLICANT: Meagher, Madeleine Joy
APPLICANT: W. Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
TILLE REFERENCE: 210121.547C1
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
NUMBER OF SEO ID NOS: 1896
SOPTWARE: FRASISEQ for Windows Version 4.0
SEQ ID NO 326
LENGTH: 439
RESULT 3
US-09-920-300A-689
Sequence 689, Application US/09920300A
Patent NO. US20020136728A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-10-033-528-326
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US-10-033-528-326/c
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Pred. No. 8.4e-103;
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                                        US-10-033-528-689
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NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 689
LENGTH: 439
                                                                                      SEQ ID NO 689
LENGTH: 439
          Query Match
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              Sequence 689, Application US/10033528 Patent No. US20020131971A1
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                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
NUMBER OF SEQ ID NOS: 1896
                                                                                                                                                                                TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: AND DIAGNOSIS OF COLON (FILE REFERENCE: 210121.547C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Meägher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547
CURRENT APPLICATION NUMBER: US/09/920,300A
                                                                                                                     SOFTWARE: FastSEQ for Windows Version
                                                        TYPE: DNA
ORGANISM: Homo
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                                                                                                                                                                                                                                              Meagher, Madeleine
Xu, Jiangchun
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                                                        sapiens
                                                                                                                                                                                                                                  Heather
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          32.7%;
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Pred. No. 2.3e-102;
0; Mismatches 2;
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          Score 416
          . 8 ;
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          DВ
          12;
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          Length 439;
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CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-88
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-04-88
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 418; Conserv
                          SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
                      NUMBER OF SEQ ID I
SOFTWARE: FastSEQ
SEQ ID NO 4064
                                                                              PRIOR APPLICATION PRIOR FILING DATE:
                                                                                                                    PRIOR APPLICATION NUMBER: 60/223,416 PRIOR FILING DATE: 2000-08-04
                                                                                                                                      PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1094
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                                                                                                                                                                            APPLICATION NUMBER: 60/222,903
                                                                                                                                                                                                               FILING DATE: 2000-05-04
APPLICATION NUMBER: 60/206,201
FILING DATE: 2000-05-22
APPLICATION NUMBER: 60/218,950
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/202,084
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                                           NOS: 9597
Q for Windows Version
                                                                                                     NUMBER:
                                                                                2000-08-07
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RESULT 7
US-10-033-528-610
US-00-033-528-610
; Sequence 610, Application US/10033528
; Patent No. US20020131971A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 610
LENGTH: 234
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Patent No. US20020136728A1
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APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madel
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 234
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 18.4%; Score 234; DB 10; Local Similarity 100.0%; Pred. No. 1.9e-53; nes 234; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                  GTGAGAGAAACCCATAAAGAGGGAAATACTATGTGAAGTATGCCGGAAAACATTT 853
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                                                                                                                                    GTGAGAGAAACCCCATAAAGAGGAAATACTATGTGAAGTATGCCCGGAAAACATTT
                                                                                                                                                                                                               TATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGGACGGAACTTCTGAAACAT
                                                                                                                                                                                                                                                                                                                             TGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACATGCCAAGGCCCACGAGGGC 739
                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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Pred. No. 1.9e-5;
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APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
ITLE REFERENCE: 210121.547C1
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
NUMBER OF SEQ ID NOS: 1896
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 510
LENGTH: 234
                                                                                                                                                                                                                                                                   APPLICANT: Burmer, Glenna C.
APPLICANT: LifeSpan BloSciences, Inc.
APPLICANT: LifeSpan BloSciences, Inc.
APPLICANT: LifeSpan BloSciences, Inc.
TITLE OF INVENTION: Nucleic Acid Sequences and
TITLE OF INVENTION: Nucleic Acid Sequences and
TITLE OF INVENTION: Number: US/09/292,758
CURRENT APPLICATION NUMBER: US/09/292,758
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION UMBER: US 60/081,887
EARLIER APPLICATION UMBER: US 60/081,887
EARLIER FILING DATE: 1998-04-15
NUMBER OF SEO ID NOS: 147
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 68
LENGTH: 362
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                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens US-09-292-758-68
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; ORGANISM: Homo sapiens
US-10-033-528-610
                                                                                                                                              Query Match
Best Local S
Matches 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 68, Application US/09292758 Publication No. US20020197602A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                             TYPE: DNA
                 1063 GCATGCTGTTGTACATGATCCTGACCAGAAGAAATGAAGCTC-AAAGTCAAAAAATCTC 1121
                                                                                           1006 TGTGTGTGAACATGCTGGCTGTGGCAAAA--CATTTGCAATGAAACAAAGTCTCAC-TAG 1062
                                                                     302
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hes 263; Conserv
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                                                                                                                                            Score 226; DB 9;
Pred. No. 3.5e-51;
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Pred. No. 1.9e-53;
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GENERAL INFORMATION:

APPLICANT: CHOO, Yen

APPLICANT: ULLMAN, Christopher G.

TITLE OF INVENTION: GENE SWITCHES

FILE REFERENCE: 8325-2003 / G7-US1

CURRENT APPLICATION NUMBER: US/09/995,973

CURRENT FILING DATE: 2002-03-19

NUMBER OF SEQ ID NOS: 59

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 947

TYPE: DNA
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US-09-995-973-2
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                                                                                             ATATATATGCAGTTTTGAAGACTGTAAGAAGACCTTTAAGAAACATCAGCAGCTGAAAAAT 627
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Pred. No. 3.6e-31;
0; Mismatches 201
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US-09-732-348-5

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TITLE OF INVENTION: Regulated Gene Expression in FILE REFERENCE: 674538-2001
CURRENT APPLICATION NUMBER: US/09/732,348
CURRENT FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 947
TYPE: DNA
ORGANISM: Artificial Sequence
 ; Sequence 1, Application US/09995973; Publication No. US20030024006A1
; GENERAL INFORMATION:
   APPLICANT: CHOO, Yen
   APPLICANT: ULLMAN, Christopher G.
   TITLE OF INVENTION: GENE SWITCHES
   FILE REFERENCE: 8325-2003 / G7-US1
; CURRENT APPLICATION NUMBER: US/09/995,973
; CURRENT FILING DATE: 2002-03-19
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APPLICANT: Yen Choc
TITLE OF INVENTION:
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LOCATION: (909)..(938)
OTHER INFORMATION: c-myc tag, other features except
OTHER INFORMATION: ted above) same as SEQ ID NO:
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LOCATION: (723)..(308)
OTHER INFORMATION: transactivation domain of VP64,
OTHER INFORMATION: listed below) same as SEQ ID NO:
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nes 273; Conservative
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Pred. No. 3.6e-31;
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; OTHER INFORMATION:
US-09-995-973-1
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US-09-732-348-4
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LENGTH: 995
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Best Local Similarity 57.6%;
                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/732,348
CURRENT FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                     FILE REFERENCE: 6
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                                                                                                                                                                    TYPE: DNA
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NAME/KEY: misc_feature
LOCATION: (16)..(416)
OTHER INFORMATION: Fingers
NAME/KEY: misc_feature
LOCATION: (308)..(416)
                                                                                   PEATURE:
NAME/KY: misc_feature
LOCATION: (15)..(17)
OTHER INFORMATION: translational
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                                                                                                                                                                                                                    PatentIn version
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NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver.
                                                 688 ACACTTTGCATCACCCAGCAAGCTGAAACGACATGCCAAGGCCCACGAGGGCTA 741
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CCGCTTTTCTCGCTCGGATGAGCTTACCCGCCATATCCGCATCCACACAGGCCA
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CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/46,731
PRIOR FILING DATE: 1994-11-21
PRIOR FILING DATE: 1994-11-21
PRIOR FILING DATE: 1994-11-21
SOFTWARE: PATCHING VET. 2.0
SEQ ID NO 5443
LENGTH: 449
                                                                                                                                                                                                                                                                                                          US-09-783-590-5443; Sequence 5443; Application; Patent No. US20020110850A1
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NAME/KEY: misc_feature
LOCATION: (417)...(689)
OTHER INFORMATION: three fingers of zinc f
NAME/KEY: misc_feature
LOCATION: (701)...(722)
OTHER INFORMATION: Nuclear Localization Si
NAME/KEY: misc_feature
LOCATION: (957)...(986)
OTHER INFORMATION: c-myc tag
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APPLICANT: Haseltin
APPLICANT: Li, Haod
APPLICANT: Rosen, C
APPLICANT: Ruben, S
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Best Local Similarity
                                                                                                                                                                                   APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences,
FILE REFERENCE: PO-16.2C1
ORGANISM: Homo sapiens
                  TYPE: DNA
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Haseltine, William
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57.6%;
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Pred. No. 3.7e-31;
0; Mismatches 201;
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Best Local Similarity
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OTHER INFORMATION: n e
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LOCATION: (181)
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                                                           TNCNTTGTGGGCAAAAACTGGGACGGGACTTCTGNAACTGTGAGNGAAACCCTTAAGGGG
                                                                             TCCTTTGTGGCAAAAACATGGACGGAACTTCTGAAACATGTGAGAGAAACCCCATAAAGAG
                                                                                                                                       AGCAAGCTGAAA--CGACATGCCAAGGCCCACGAGGGCTATGTATG-TCAAAAAGGATGT
                                                                                                                     AGCAAGCTGNAAACGGACATGCCAAGGCCCACGAGGGTTATGTATGTTCAAAAAGGNTGT
                                                                                                                                                                                                                                                                           -GAAGACCTTTAAGAAA-----CATCAGCAGCTGAAAATCCATCAGTGCCAGCATACCAA 648
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Pred. No. 1.9e-28;
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Indels Length

Gaps

11;

422 820 760 302 703 242

362

449; 17;

DB 10; Length 368

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US-09-920-300A-1747/c
; Sequence 1747, Application US/09920300A
; Patent No. US20020136728A1
; NAME/KEY: misc_feature
; LOCATION: 223, 323
; OTHER INFORMATION: n =
US-09-920-300A-1747
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; LOCATION: (1)...(1111)
; OTHER INFORMATION: n - A,T,C
US-09-833-381-1175
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US-09-833-381-1175
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APPLICANT: ROBISON, Keith E.

APPLICANT: ROBISON, No. US20020132090Alel Nucleic Acid and Protein Homologs

TITLE OF INVENTION: No. US20020132090Alel Nucleic Acid and Protein Homologs

FILE REFERENCE: 5800-119

CURRENT APPLICATION NUMBER: US/09/833,381

CURRENT FILING DATE: 2001-04-11

PRIOR APPLICATION NUMBER: 09/516,448

PRIOR APPLICATION NUMBER: 09/516,448

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 2050

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1175

TENERS THE NUMBER OF SEC ID NOS: 2050

SEQ ID NO 1175

LENGTH: 1111
                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILTMS DATE: 2001-07-31
NUMBER OF SEO ID NOS: 1789
SOFTWARE: FASTSEQ for Windows Version 4.0
SEO ID NO 1747
LENGTH: 368
TYPE: DNA
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Best Local Similarity 61.1%;
Matches 140; Conservative
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                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.547
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
                                                                                                     ORGANISM: Homo sapiens FEATURE:
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Pred. No. 1.9e-13; 
0; Mismatches 89; Indels 0;
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Search completed: February 10, 2003, 12:58:32 Job time : \$1.105 secs
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Best Local Similarity 98.8%;
                                                                  797 CATGTGAGAGAAACCCATAAAG
                                                                                                     737 GGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGGACGGAACTTCTGAAA 796
                                                    296 CATGTGAGAGAAACCCATAAAG
                                                                                                                                                        81;
                                                                                                                                                        Conservative
                                                    275
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                                                                                                                                                       0; Mismatches
                                                                                                                                                                   Score 81; DB 10;
Pred. No. 3.1e-12;
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Sequence Sequence Sequence Sequence

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Sequence

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Post-processing: Minimum Match 0%
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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                       GenCore version
(c) 1993 - 2003
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Compugen Ltd
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LOCATION: 20..1288
LOCATION ETHOD:
JENTIFICATION METHOD:
US-08-523-376-2
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Query Match
Best Local Similarity
                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1399 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & STREET: 2100 Pennsylvania Avenue, N.W.
                                                                                                                              IMMEDIATE SOURCE:
LIBRARY: human
CLONE: OTK7
                                                                                                                  FEATURE:
                                                                                                                                                                            TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: I
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 536
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20037-3202
                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                              : human fetal brain cDNA OTK7
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Sadahito, HTFIIIA GENE
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Kouichi, OZAKI
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Satoshi, TAKEDA
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US-08-93-911-1
PCT-US-9-04-67-1
US-08-234-78-3
US-08-25-05-23-3
US-08-102-942A-3
US-08-102-942A-3
US-08-102-942A-3
US-08-102-942A-3
US-08-726-214-1
US-08-726-214-1
US-08-726-237-7
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US-09-385-028-20
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US-08-46-382-3
     Score 1231.6; DB 1;
Pred. No. 3.9e-312;
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                  Length 1399;
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Result

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Query

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1231.6 1228.6 63.2 61.4 58.8 54.8 53.2 53.2 53.2

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Database

Minimum DB

Scoring table: Sequence: Title: Perfect score: Run

Matches

Conservative

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1039 TGGCTGTGGCAAAACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGA
              TGGCTGTGGCAAAACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGA
                                                                                                                                                                                                                                                                                                                        CAAGTGTACCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACA 720
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TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1269 base pairs
                                                                                                                                                Query Match
Best Local Similarity
Matches 1264; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08523376 Patent No. 5808030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 293-7060
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sadahito, SIN TITLE OF INVENTION: hTFIIIA GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 2100 Penn
CITY: Washington
STATE: D.C.
COUNTRY: United S
              121
                                         61
                                                                   61
                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20037-3202
                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/523,376
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                                                                                                          TTACCCTTGGCTAA 1291
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              ACCTGTCTCGGCACGTGGCAGCGCGCCTGGCCCTGGGCTTGGAGGCGCCGGCCCCTGGA
                                      GTGCCGGCGTCGCGAAGGTTCAGCAGGGAGCCGTGGGCCGGGCGCG-CGGTTCCCGGC
                                                                   TTACCCTTGGCTAA 1273
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2100 Pennsylvania Avenue,
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Yoshikazu, SHIM
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                                                                                                                                               Score 1228.6; DB 1;
Pred. No. 2.3e-311;
0; Mismatches 4;
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                                                                                                                TCCTGACAAGAAGAAAATGAAGCTCAAAGTCAAAAAATCTCGTGAAAAAAC-GGAGTTTGG
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GTCAAAACGGAGAGTCACCCAACTGTGTGGAAGACAAGATGCTCTCGACAGTTGCAGTAC
                                                                                                    TCCTGACAAGAAGAAAATGAAGCTCAAAGTCAAAAATCTCGTGAAAAAACGGGAGTTTGG
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; LENGTH: 1471
; TYPE: DNA
; ORGANISM: mouse
US-09-492-985-11
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US-09-492-985-11
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 11
                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                               Sequence 1, Application US/09492985
Patent No. 6376240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Best Local Similarity 48.9%;
APPLICANT: Song, An M.
APPLICANT: Chen, Ya-Fen
APPLICANT: KIENSKY, ALAN M.
TITLE OF INVENTION: RFLAT-1: A Transcription Factor That
TITLE OF INVENTION: ACCIVATES RANTES Gene Expression
FILE REFERENCE: SUN-1113P
CURRENT APPLICATION NUMBER: US/09/492,985
CURRENT FILING DATE: 2000-01-27
EARLIER APPLICATION NUMBER: 60/117,576
EARLIER FILING DATE: 1999-01-27
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APPLICANT: Chen, Ya-Fen
APPLICANT: Krensky, Alan M.
TITLE OF INVENTION: RFLAT-1: A Transcription Factor That
TITLE OF INVENTION: Activates RANTES Gene Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/492,985
CURRENT FILING DATE: 2000-01-27
EARLIER APPLICATION NUMBER: 60/117,576
EARLIER FILING DATE: 1999-01-27
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Pred. No. 4.2e-07;
0; Mismatches 178;
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                                                                                   ; NAME/KEY: CDS
; LOCATION: (82)..(1710)
US-09-362-123A-3
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                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/362,123A
CURRENT FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: 09/128,310
PRIOR FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 2992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09362123A Patent No. 6451558 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.8%;
Best Local Similarity 48.9%;
Matches 193; Conservation
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SOFTWARE: FRASLSEQ for Windows Version
SEQ ID NO 1
LENGTH: 1430
                      Query Match
Best Local Similarity
    Matches
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cooke, Michael Paul
APPLICANT: Holness, Claire
APPLICANT: Sirenko, Oksana
TITLE OF INVENTION: NO. 6451558el Genes in
FILE REFERENCE: 4-30629A/SYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: homo sapien FEATURE:
                                                                                                                                                 FEATURE:
                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCAATTACAGCAAAGCCTGGAAGCTTGACGCGCACCTGTGCAAGCACACGGGGGAGAGA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGCCGGGGCCCGGGGAGCGGGCGAGCCCGGCCTCAGACAAAGGGTCCGGCGGGGCCGA 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGTCGCTGTCGTCCTTGACCATCGCCGACGCGTTCATTGCAGCCGGCGAGAGCTCAGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGCCCCCAGCCCGGCGTGGAGCGAGCCGGAGCCCGAGGCGGGCTGGAGCCCGAGCGG 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGCGCCTGGGCTTGGAGGCGCGCGCGCCC-TGGATCCGCCGGCCGTGGTCGCC 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCTTCGCCTGCAGCTGGCAGGACTGCAACAAGAAGTTCGCGCGCTCCGACGAGCTGGCG 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTCGCCCCGACCTCGAGTCCCCGCAGAGGAAGCACAAGTGCCACTACGCGGGCTGCGAG 903
    142;
    Conservative
                      4.6%;
54.6%;
    0,
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Score 58.8; DB 4;
Pred. No. 8e-06;
0; Mismatches 112;
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                                                                                                                                                                                                                                                                                                                                                                                             Control of Hematopoiesis
                                       Length 2992;
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    Indels
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US-08-570-227A-1
US-08-570-227A-1
Sequence 1, Application US/08570227A
PALENT NO. 5981217
GENERAL INFORMATION:
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; LOCATION: (0)...(0)
; OTHER INFORMATION: Zic 1 Protein gene; Genbank Accession D76435
US-09-234-332-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : SEQ ID NO 5
: LENGTH: 3138
: TYPE: DNA
: ORGANISM: Human
: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/234,332A
CURRENT FILING DATE: 1999-01-20
NUMBER OF SEO ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: CONVERSION OF NON-NEURONAL CELLS TITLE OF INVENTION: NEURONS; TRANSDIFFERENTIATION OF FILE REFERENCE: P07 41494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                               1822
                                                                                                                                                                                                                                                                                                                                               1702 GGCTGTGGCAAGGTCTTCGCGCGCTCCGAGAATTTAAAGATCCACAAAAGGACGCACACA 1761
                                                                                                                                                                                                                                                                                                                                                                                                                                        1642 AAACTGGTTAACCACATCCGCGTGCACACGGGCGAGAAGCCCTTTCCCTTTCCCTT 1701
                                                                                                                                                                                                                                                                                                                                                                                              401
                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 4.3%;
Local Similarity 55.2%;
                                                                                                                                                                                                        AACTTGAAGAAACA 534
                                                                                                                                                                                                                                                                                                   GGAGAAAAGCCGTTTGTTGTGCAGCCACTGGCTGTGATCAAAAATTCAACACAAAATCA 520
                                                                                                                                                                                                                                                                                                                                                                                         GGGTGTGGCAAGGCCTTCATCAGGGACTACCATCTGAGCCGCCACATTCTGACTCACACA 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCAGCCGGCGAGAGCTCAGCTCCGACCCCGCGCGCCCCGCGCTTCCCAGGAGGTTCAT
                                                                                                                                                               GACCGCAAGAAGCA 1835
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                                                                                                                                                                                                                                                       GGGGAGAAGCCCTTCAAGTGCGAGTTTGAGGGCTGTGACCGGCGCTTCGCTAACAGCAGC 1821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54.8; DB 3; LL.,
Pred. No. 9.1e-05;
""amatches 87; Indels
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APPLICANT:

Subramaniam,

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US-09-077-991-1
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                                                                                                               Sequence 1, Application US/09077991
Patent NO. 6207375
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.28;
Best Local Similarity 54.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
APPLICANT: Subramaniam, M.
APPLICANT: Spelsberg, T.C.
APPLICANT: Roche, P.C.
TITLE OF INVENTION: TGF-Beta inducible early factor-1
TITLE OF INVENTION: (TIEF-1) and a method to detect breast cancer
FILE REFERENCE: 150.157US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2881 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: WOESENEY, WATTEN D
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 151
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-359-3260
                                                                                                                                                                                                                                                                                                                                                                                                1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                 1365 AAGAAATTTGCGTG 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1185 AGGAGTCACATCTGTAGCCACCCAGGATGTGGCAAGACATACTTTAAAAGTTCCCATCTG 1244
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                    467 AAGCCGTTTGTTTG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                347 GACGCGCACCTGTGCAAGCACACGGGGGAGAGACCATTTGTTGTGACTATGAAGGGTGT 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287 AGGAGGTTCATCTGCTCCTTCCCTGACTGCAGCGCCAATTACAGCAAAGCCTGGAAGCTT 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 11-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                      GAAAGGAGGTTTGCCCGTTCTGATGAACTGTCCAGACACAGGCGAACCCCACACGGGTGAG 136
                                                                                                                                                                                                                                                                                                                                                          GGCAAGGCCTTCATCAGGGACTACCATCTGAGCCGCCACATTCTGACTCACACAGGAGAA 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
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BY OSTEOBLASTS
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Pred. No. 0.00023;
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; SEQ ID NO 1
; LENGTH: 2881
; TYPE: DNA
; ORCANISM: Homo sapiens
US-09-077-991-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 13 SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: US 08/570,227 EARLIER FILING DATE: 1995-12-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: PCT/US96/19555
EARLIER FILING DATE: 1996-12-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/077,991
CURRENT FILING DATE: 1998-07-07
             FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER,
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECON
                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         467
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                                                                                                                                                                                                                                                                                                                                                                                   ZIP:
                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                FILING DATE:
                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1800 Dia
CITY: Alexandria
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGGCCCACACGAGGACGCACACAGGAGAAAAGCCTTTCAGCTGTAGCTGGAAAGGTTGT 130
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Similarity 54.6%;
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1800 Diagonal Road
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(703)683-4109
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Pred. No. 0.00023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suite
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US-09-657-042A-3
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US-08-232-463-14
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                                                                                                                                                                                                                                 SEQ ID NO 3
LENGTH: 3600
                                                                  Matches
                                                                                             Query Match
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                                                                                                                                                                                                                                                           FILE REFERENCE: RTS-0148
CURRENT APPLICATION NUMBER: US/09/657,042A
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 88
                                                                                                                                                                                                                                                                                                                                                APPLICANT: C. Frank Ben
APPLICANT: Jacqueline Wyatt
                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341 AAGCTTGACGCGCACCTGTGCAAGCACACGGGGGAGAGACCATTTGTTGTGACTATGAA 400
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                                                                  Local Similarity
nes 149; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.1%; Score 52.8; DB 1; Length 7218; Local Similarity 4.5%; Pred. No. 0.00043; Local Similarity 4.5%; Pred. No. 0.00043; Indels 0 hes 18; Conservative 218; Mismatches 160; Indels 0
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ATGCTGGTGGTTCACATGCGCAGACACACTGGCGAGAAGCCACACAAGTGCACGTTTGAA 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TANGCAACACATGAAAACTCATGCCCCAGAAAGGGA 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCATAAAGAGGAAATACTATGTGAAGTATGCCGGAAAACATTTAAACGCAAAGATTACCT 870
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                                                                  Conservative
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                                                                                4.18;
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                                                                                                                                                                                                                                                                                                                                ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-1 EXPRES
                                                               Score 52.6; DB 4;
Pred. No. 0.00036;
0; Mismatches 139;
                                                                                                Length 3600;
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CORRESPONDENCE ADDRESS

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RESULT 12
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US-09-907-843-3
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APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
                                                                                                          Sequence 1, Application US/08946241B Patent No. 5928941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09907843 Patent No. 6440739
GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: McA'Nulty, Megan M
TITLE OF INVENTION: REPRESSOR
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/907,843
CURRENT FILING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-2 EXPRESSIO FILE REFERENCE: RTS-0279
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: (57)
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                         REPRESSOR KRUPPEL-LIKE FACTOR
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STREET: L. BOSTON

225 Franklin Street

Fish & Richardson P.C.

ADDRESSEE:

COUNTRY:

USA

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                                                                                                                                                                                                                       Sequence 8, Application US/08946241B
Patent No. 5928941
GENERAL INFORMATION:
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OPERATING SYSTEM: DOS
SOETWARR: FASTSEQ Version 2.0
SOETWARR: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/946,241B
FILING DATE: 07-OCT-1997
PRIOR APPLICATION NUMBER: 60/030,035
APPLICATION NUMBER: 60/030,035
FILING DATE: 05-NOV-1996
APPLICATION NUMBER: 60/027,521
FILING DATE: 07-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                 APPLICANT: Lee, Mu-En
APPLICANT: MCA'Nulty, Megan M.
TITLE OF INVENTION: REPRESSOR
                                                                                                                                                                                                                                                                                                                                           1714 ATTCGCCCGCTCAGATGAACTGACCAGGCACTACCGTAAACACACGGGGCACCGCCGTT 1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,
COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1594 CACTTGTGATTACGCGGGCTGCGGCAAAACCTACACAAAGAGTTCCCATCTCAAGGCACA 1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                               415 CTTCATCAGGGACTACCATCTGAGCGCGCCACATTCTGACTCACACAGGAGAAAAGCCGTT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                  355 CCTGTGCAAGCACACGGGGAGAGACCATTTGTTTGTGAACTATGAAGGGTGTGGCAAGGC 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 CATCTGCTCCCTTGCCTGACTGCAGCGCCAATTACAGCAAAGCCTTGAAGCTTGACGCGCA 354
                                   COUNTRY: USA
ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 054
                                                                    STATE:
                                                                                       CITY:
                                                                                                  ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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                                                                                     Boston
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EDNESS: single
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 Diskette
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55.0%;
                                                                                                                                                                       REPRESSOR KRUPPEL-LIKE FACTOR
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RESULT 14
US-09-309-053-1
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                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09309053
Patent No. 6077933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/030,035
APPLICATION NUMBER: 60/030,035
FILING DATE: 05-NOV-1996
APPLICATION NUMBER: 60/027,521
TTING DATE: 07-027-1996
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                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: McA'NULty, Megan M.
TITLE OF INVENTION: REPRESSOR KRUPPEL-LIKE FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1889 base pairs
                                                            SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
                FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        1714 ATTCGCCCGCTCAGATGAACTGACCAGGCACTACCGTAAACACACGGGGCACCGCCCGTT 1773
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                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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TELEFAX: 200154
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                                                                                          OPERATING SYSTEM:
                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                          ADDRESSEE: FISH & N. STREET: 225 Franklin Street
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 APPLICATION NUMBER:
                                                                                                           COMPUTER:
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                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTCATCAGGGACTACCATCTGAGCCGCCACATTCTGACTCACACAGGAGAAAAGCCGTT 474
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                                                                                                                                                                      USA
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                                                                                                        IBM Compatible
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                                               US/09/309,053
08/946,241
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APPLICATION NUMBER:

07-OCT-1997

60/030,035

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; LOCATION:
US-09-309-053-1
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Patent No. 6077933

GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: MCA Multy, Megan M.
TITLE OF INVENTION: REPRESSOR KRUPPEL-LIKE FACTOR
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 99; Conserv
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NAME: Creason, Gary L.
REGISTRATION UNMER: 34,310
REFERENCE/DOCKET NUMBER: 0543
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-8906
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INFORMATION FOR SEQ ID NO:
                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/946,241
FILING DATE: 07-0CT-1997
FILING DATE: 07-0CT-1997
                                                                                                                                                                            COMPUTER: IRM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastEQ Version 2.0
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1594 CACTTGTGATTACGCGGGCTGCGGCAAAACCTACACAAAGAGTTCCCCATCTCAAGGCACA 1653
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APPLICATION NUMBER: 60/027,521
TITING DATE: 07-0CT-1996
             APPLICATION NUMBER: 60/030,035
ETILING DATE: 05-NOV-1996
APPLICATION NUMBER: 60/027,521
FILING DATE: 07-OCT-1996
                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: FISH .... Street
                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                               STATE:
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                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                          COUNTRY: USA
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 Mismatches

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Search completed: February 10, 2003, 12:47:09 Job time: 111.743 secs
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                                                                                                                                                                                                                                                                                                           Query Match
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 054
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                  1714 ATTCGCCCGCTCAGATGAACTGACCAGGCACTACCGTAAACACACGGGGCACCGCCCGTT 1773
                                                                                                                                                                                                        1594 CACTTGTGATTACGCGGGCTGCGGCAAAACCTACACAAAGAGTTCCCATCTCAAGGCACA 1653
                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1889 base pairs
                                                                                                                                     355 CCTGTGCAAGCACACGGGGGAGAGACCATTTGTTTGTGACTATGAAGGGTGTGGCAAGGC 414
                                                                                                    415 CTTCATCAGGGACTACCATCTGAGCCGCCACATTCTGACTCACACAGGAGAAAAGCCGTT 474
                                                                                                                                                                                                                                        295 CATCTGCTCCCTGACTGCAGCGCCAATTACAGCAAAGCCTGGAAGCTTGACGCGCA 354
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                                                                                                                                                                                                                                                                                              Local
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                            4.0%;
Similarity 55.0%;
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                                                                                                                                                                                                                                                                                                           DB 3;
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Database
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Maximum DB
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Perfect score:
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seq length: 2000000000
  Gapop 10.0 , Gapext 1
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1273
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                          Cgn2_6/ptodata/1/pna/US08_COMB.seq: *
(cgn2_6/ptodata/1/pna/US08_COMB.seq: *
(cgn2_6/ptodata/1/pna/US09_COMB.seq: *
(cgn2_6/ptodata/1/p
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|: /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 18066, A Sequence 24482, A	3560,	3560,	Ü	1661	Sequence 4, Appli	_		Sequence 16829, A			1322,	Sequence 1934, Ap	10703,	Sequence 8862, Ap	960	ω •	Sequence 1, Appli	Sequence 3, Appli	Sequence 1, Appli	Description		

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RESULT 1

US-09-831-426-1

Sequence 1, Application US/09831426

GENERAL INFORMATION:

APPLICANT: Hoechst Marion Roussel
APPLICANT: Bordon-Pallier, F.

APPLICANT: Rocher, C.

TITLE OF INVENTION: Human htFIIIA gene and coc
FILE REFERENCE: 146.1364

CURRENT FILING DATE: 2001-05-08

NUMBER OF SEQ ID NOS: 10

SOFTMARE: Patentin Vers. 2.0

SEQ ID NO 1

LENGTH: 1273

TYPE: DNA
ORGANISM: Human
FEATURE:
NAMEXKEY: CDS
LOCATION: (176)...(1270)

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US-09-652-814-873-10092

US-09-644-873-7415

PCT-US01-8569-903

US-10-264-049-803

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US-09-306-609-4878

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US-09-326-600-4878

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US-09-326-326-326

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APPLICANT: Bordon-Pallier, F.
APPLICANT: Bordon-Pallier, F.
APPLICANT: Rocher, C.
TITLE OF INVENTION: Human htFIIIA gene and coded htFIIIA protein
FILE REFERENCE: 146.1364
CURRENT APPLICATION UNBER: US/09/831,426
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 10
SOFTMARE: PatentIN Vers. 2.0
SEQ ID NO 3
LENGTH: 1273
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CURRENT APPLICATION NUMBER: U5/09/831,426C
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 10
SOFTMARE: Patentin Vers. 2.0
SEQ ID NO 1
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APPLICANT: Bordon-Pallier, F.
APPLICANT: Rocher, C.
                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
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APPLICANT: Hoechst Marion Roussel
APPLICANT: Bordon-Pallier, F.
APPLICANT: Bordon-Pallier, F.
APPLICANT: Rocher, C.
TITLE OF INVENTION: Human htFIIA gene and coded htl
FILE REFERENCE: 146.364
CURRENT APPLICATION UNMBER: US/09/831,426C
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEO ID NOS: 10
SOFTWARE: Patentin Vers. 2.0
SEQ ID NO 3
LENGTH: 1273
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ORGANISM: Human
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Sequence 9602, Application US/09644868
GENERAL INFORMATION:
APPLICANT: White, David
APPLICANT: White, David
APPLICANT: HOITEMAN, DOUGLAS A.
APPLICANT: PAN, YANG
TITLE OF INVENTION: NOVEL NUCLEIC ACID INTERESTOR
FILE REFERENCE: 1600,1168-001
CURRENT FILING DATE: 2000-08-28
CURRENT FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: 60/151,063
PRIOR APPLICATION NUMBER: 50/151,063
PRIOR PILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 10075
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 9602
LENGTH: 1597
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
LOCATION: (1):..(1597)
OTHER INFORMATION: n - A,T,C or G
US-09-644-868-9602
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US-09-644-868-9602
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Sequence 8862, Application US/09652126
GENERAL INFORMATION:
APPLICANT: SDyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: THEREFOR FILE REFERENCE: 1600.1185-001
CURRENT APPLICATION NUMBER: US/09/652,126
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,132
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 10051
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8862
SEQ ID NO 8862
LENGTH: 1597
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US-09-652-126-8862
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature
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RESULT 7

US-09-652-814-10703
Sequence 10703, Application US/09652814
Sequence 10703, Application US/09652814
GENERAL INFORMATION:
APPLICANT: HOLTZMAN, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID PRICE OF INVENTION: THEREFOR THILE REFERENCE: 1600.1191-001
CURRENT APPLICATION NUMBER: US/09/652,814
CURRENT APPLICATION NUMBER: 60/152,109

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                                           TCAAAACGGAGAGTCACCCAACTGTGTGGAAGACAAGATGCTCTCGACAGTTGCAGTACT
                                                                                      CTCTCATCTCAGTGGATATATCCCTCCCAAAAGGAAACAAGGGCAAGGCTTATCTTTGTG
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PRIOR FILING DATE: 1999-08-31

NUMBER OF SEO ID NOS: 10797

SOFTWARE: FASTSEO for Windows V

SEQ ID NO 10703

LENGTH: 1597

TYPE: DNA

ORGANISM: HOMO SAPIENS
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1597)
OTHER INFORMATION: n - A,T,C OI
US-09-652-814-10703
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                                                TGCCAAGGCCCACGAGGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATG
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                                        TGCCAAGGCCCACGAGGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATG
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Pred. No. 1.1e-278;
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SEQ ID NO 1934

LENGTH: 1597

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1597)
OTHER INFORMATION: n = A
US-09-716-473-1934
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                                                                                                                                   Best Local Similarity Matches 1271; Conserv
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TITLE OF INVENTION: NOVEL NUCLEIC ACI
TITLE OF INVENTION: THEREFORE
FILE REFERENCE: 1600.2043-001
CURRENT APPLICATION NUMBER: US/09/716,
CURRENT FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/166,502
PRIOR FILING DATE: 199-11-19
NUMBER OF SEQ ID NOS: 293
SOFTWARE: FastSEQ for Windows Versio
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Pred. No. 1.1e
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; ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc_feature LOCATION: (1)...(1597) OTHER INFORMATION: n • A US-09-716-990-1322
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APPLICANT: HOILTMAN, DOUGLAS A.
APPLICANT: HOILTMAN, DOUGLAS A.
APPLICANT: HOILTMAN, DOUGLAS A.
APPLICANTION: HOVEL NUCLEIC ACID MOI
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600,2039-001
CURRENT APPLICATION NUMBER: US/09/716,990
CURRENT FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: US 60/166,926
PRIOR FILING DATE: 1999-11-22
NUMBER OF SEG ID NOS: 1691
SOFTWARE: FASTSEQ for Windows Version 4.0
SEG ID NO 1322
LENGTH: 1597
TYPE: DNA
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TGCAGCCACTGGCTGTGATCAAAAATTCAACACAAAATCAAACTTGAAGAAACATTTTGA
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Pred. No. 1.1e-278;
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Sequence 6336 Application US/09721589
GEMERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Villeval, Jean-Luc
TITLE OF INVENTION: NOVEL NUCLEIC ACID METALLE OF INVENTION: THEREFOR FILE REFERENCE: 1600.2045-001
CURRENT APPLICATION NUMBER: US/09/721.589
CURRENT FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/167,380
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 7017
SOFTWARE: FASTSEQ for Windows Version 4.
SEQ ID NO 6336
LENGTH: 1597
TYPE: DNA
ORGANISM: Homo sapiens
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  FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1597)
OTHER INFORMATION: n =
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                                               GACGGAACTTCTGAAACATGTGAGAGAAACCCATAAAGAGGAAATACTATGTGAAGTATG
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Pred. No. 1.1e
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GTGCCGGCGTCGCGCGAAGGTTCAGCAGGGAGCCGTGGGCCGGCGGCGGCCGGTTCCCGGC 120
                                                          .8; DB 2:
1.1e-278;
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APPLICANT: Genting, David P.
APPLICANT: Kingsbury, Gillian A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: THEREFOR FILE REFERENCE: 1600,2051-001
CURRENT APPLICATION NUMBER: US/09/726,788
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/168,131
PRIOR FILING DATE: 199-11-30
NUMBER OF SEQ ID NOS: 7691
SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0
SEQ ID NO 6896
LENGTH: 1597
TYPE: DNA
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: LOCATION: (1)...(1597)
: OTHER INFORMATION: n =
US-09-726-788-6896
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US-09-726-788-6896
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Best Local Similarity
Matches 1271; Conserv
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Pred. No. 1.1e-278;
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Sequence 16829, Application US/60324185
GENERAL INFORMATION:
APPLICANT: Mortis, MacDonald
APPLICANT: Lal, Preeti
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                                       TCAAAACGGAGAGTCACCCAACTGTGGGAAGACAAGATGCTCTCGACAGTTGCAGTACT 1260
                                                                                CTCTCATCTCAGTGGATATATCCCTCCCAAAAGGAAACAAGGGCAAGGCTTATCTTTGTG
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; OTHER INFORMATION: Incyte ID NAME/KEY: UNSURE : LOCATION: 2351 ; OTHER INFORMATION: a, t, c, g US-60-324-185-16829
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CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 35862
SOFTWARE: PERL Program
SEQ ID NO 16829
LENGTH: 2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 1270; Conserv
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Best Local :
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TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
FILE REFERENCE: GX-0019-1 P
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NAME/KEY: misc_feature
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                                                                                                           GTGCAGCCACTGGCTGTGATCAAAAATTCAACACAAAATCAAACTTGAAGAAACATTTTG
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          TCAAGTGTACCCAGGAAGGATGTGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGAC
                                                                                                                                                                                                                                                                                             GCTCCTTCCCTGACTGCAGCGCCAATTACAGCAAAGCCTGGAAGCTTGACGCGCACCTGT
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                                                                                               AACGCAAACATGAAAATCAACAAAAACAATATATATGCAGTTTTGAAGACTGTAAGAAGA
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APPLICANT: Morris, MacDonald
APPLICANT: Lial, Preeti
APPLICANT: Liep, Dinh
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Identific
TITLE OF INVENTION: MOMBER: US/60/172,373
CURRENT APPLICATION NUMBER: US/60/172,373
CURRENT FILING DATE: 199-12-16
NUMBER OF SED ID NOS: 25,772
SEQ ID NO 18068
LENGTH: 1527
TYPE: DNA
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                                                                    ; OTHER INFORMATION: US-60-172-373-18068
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 Matches 1269;
                Query Match
Best Local Similarity
                                                                                                    NAME/KEY: unsure
LOCATION: 1504, 1508
                                                                                                                                         FEATURE:
                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                         NAME/KEY: misc_feature
                                                                                                                                                                                           FEATURE:
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              Score 1222.6; DB 6
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Mismatches
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                                 DB 61;
Indels
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Gaps
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APPLICANT: Hoechst Marion Roussel
APPLICANT: Hoechst Marion Roussel
APPLICANT: Rocher, C.
APPLICANT: Rocher, C.
FILE REFERENCE: 146.1544
CURRENT APPLICATION NUMBER: US/09/831,426
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Vers. 2.0
SEQ ID NO 4
LENGTH: 1213
TYPE: DNA
JORGANISM: Human
US-09-831-426-4
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US-09-831-426-4
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APPLICANT: Hoechst Marion Roussel; APPLICANT: Bordon-Pallier, F.; APPLICANT: Rocher, C.; TITLE OF INVENTION: Human htFIIIA gene and co: TITLE OF INVENTION: Human htFIIIA gene and co: CURRENT APPLICATION NUMBER: US/09/831,426C; CURRENT FILING DATE: 2001-05-08; NUMBER OF SED ID NOS: 10.
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